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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein . protein search, using sw model

8, 2002, 19:24:14; Search time 15.0327 Seconds (without alignments) 1470.857 Million cell updates/sec November Run on:

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT 2
T05430
Hypotherical protein F28A23.180 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 24-Nov-1999
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 24-Nov-1999
C;CAccession: T05430
R;Bevan, M.; Weichselgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A. submitted to the Protein Sequence Database, October 1998
A;Reference number: 215415
A;Accession: T05430
A;Wolecule type: DNA
A;Residues: 1-917 <BEV>
A;Cross references: EMBL:AL021961
A;Experimental source: cultivar Columbia; BAC clone F28A23

DNA-(apurinic or a	probable endonucle	A/G-specific adeni	adenine glycosylas	adenine diycosylas	DNA-(apurinic or a	cystatin D precurs	endonuclease III X	endonuclease III p	endonuclease III -	endonuclease III -	endonuclease III [		OGG1 protein - yea	endonuclease III C	A / G specific ade
510860	G96984	B38535	E91108	H85953	A64479	A47142	E82780	н83208	F72387	D70316	AE3104	F98182	S49801	B81407	G83003
ç	~	7	~	~	7	7	7	7	7	7	7	~	7	~	7
209	211	350	350	350	220	142	218	212	213	220	236	260	376	208	355
8.8	8.7	8.5	8.5	8.5	8.4	8.3	8.3	8.2	8.2	8.2	8.2	8.2	8.2	8.1	8.1
61	60.5	59	59	59	58.5	57.5	57.5	56.5	56.5	56.5	56.5	56.5	56.5	26	26
30	31	32	33	34	35	36	37	38	39	40	4.1	42	43	44	45

## ALIGNMENTS

α. ..

AT2G36490

098306 098306;

RESULT 2 992360

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Mewes H.W., Mayer K., Schueller C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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SMART; SM00478; ENDO3C; 1.
SMART; SM00525; FES; 1.
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Best Local Similarity
Matches 43; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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STRAIN—CV. COLUMBIA;

MEDLINE—20083487; PubMed—10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Fuji C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.E., Umman L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

Sequence and analysis of chromosome 2 of the plant Arabidopsis

thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
F28A23.180 OR AT4634060.
Arabidopsis thaliana (Molse-ear cress).
Eukaryota: Viridiplantae/ Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae; eurosids III Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KVXXDXXTXXXWXXL-----XXXXDXXXXXXXXXXERXXEXXXEXXXXIXRWXXXQGXR 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%; Score 163.5; DB 10; Length 1207; 43.4%; Pred. No. 9.7e-20; tive 0; Mismatches 47; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135916 MW; ADDB6C9EE94DDF67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AC006919; AAD24633.1; -. InterPro; IPR003451; FeS_bind. SMART; SM00525; FES; 1. SMART; SM00525; FES; 1. SEQUENCE 1207 AA; 135916 MW; ADDB6C9EE94DDF67 CRC64;
                                                                                                                                                                                                                                                                                                 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 560 RFTPWKGSVVDSVVGVFLTQNVSDHLSSSAFMSLASQFP 598
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                  917 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
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nes 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 402:761-768(1999).
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                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                              At2g36490 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-3702;
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Query Match

Matches

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Arabidopsis thaliana (Mouse-ear Cress).

Bukaryota, Whiridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418 KVNLDPETIKEWDVLMVNDSPSRSYDDKETEAKWKKEREIFQTRIDLFINRMHRLQGNRK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bevan M., Terron N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W. Rudd S., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 33; Indels 9;
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 917;
                                  Dauner D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        017 AA; 112139 MW; 4F7C313A891EC83F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021961; CAA17565.1; -.
EMBL; AL161984; CAB80123.1; -.
InterPro; IFR002265; Endo_3c.
InterPro; IFR003651; FeS_blnd.
SEQUENCE FEON N.A. Westmann B., Granderath K., Dauner I weichselgarther M., Fartmann B., Mayer K.F.X.;
Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MRR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEOUENCE 917 AA; 106310 MW; 302B3770ACE1A454 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-200d (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 112.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.9%; Score 162; DB 10; 43.9%; Pred. No. 1.3e-19; tive 0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478 FKOWKGSVVDSVVGVFLTONTTDYLSSNAFMSVAAKFP 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 FXXWKGBVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
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5

RESULT 5

Dauner D.,

Meichselgartner M., Fartmann B., Granderath K., Dauner S., Neumann S., Hohelsel J., Jesse T., Heijnen L., Vos P.,

AFOUENCE FROM N.A.

NCBI\_TaxID=3702;

049498

RESULT 3 049498

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C: Species: Methanobacterium thermoautotrophicum (strain Delta H)
C: Species: Methanobacterium thermoautotrophicum
C: Species: Methanobacterium thermoautotrophicum
C: Species: Methanobacterium thermoautotrophicum
C: Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Jul-1999
C; Accession: B69202
R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicalire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, K.; S.; Church, G.M.; Daniels, C.J.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, K.; S.; Church, G.M.; Daniels, C.J.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, K.; S.; Church, G.M.; Daniels, C.J.; Methanobacterium thermoautotrophicum Delta H.; fu A; Reference number: A69000; MuID:99037514; PMID:9371463
A; Accession: B69202
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-233 <MTH>
A; Residues: 1-233 <MTH>
A; Residues: 1-233 <MTH>
A; Residues: 1-233 <MTH>
A; Residues: 1-234 <MTH>
A; Cross-references: GB:AE000855; GB:AE000666; NID:92621852; PIDN:AAB85267.1; PID:9262
A; Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable endonuclease III - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: 14-Aqq-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: F71025
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se R;Kawarabayasi, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000 AIID:98344137; PMID:98344137; PMID:9834
                                                                                                             A;Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49586.1; PID:g545 A;Experimental source: strain Orsay C;Genetics: A;Genetics: A;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Cyperfamily: apurinic/apyrimidinic endonuclease III C;Keywords: 4Fe-4S; metalloprotein C;Keywords: 4Fe-4S; metalloprotein F;195,202,205,211/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.4%; Score 86; DB 2; Ler Best Local Similarity 26.9%; Pred. No. 1.2e-05; Matches 29; Conservative 11; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.0%; Score 83.5; DB 2;
Best Local Similarity 26.9%; Pred. No. 3.1e-05;
Matches 29; Conservative 10; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: MTH764
A;Start codon: TTG
C;Superfamily: apurinic/apyrimidinic endonuclease III
                                                                                        A; Residues: 1-222 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endonuclease III family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
E;Accession: G87530
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
D, J; Ermolaeva, M.; White, O.; Salaberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-414, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87530
A;Scatus: preliminary
A;Accessious: GB:AE005673; NID:913423785; PIDN:AAK24243.1; GSPDB:GN00148
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: A75109
R;Anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
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                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-265 <STO>
A;Cross-references: GB:AE004437; NID:g10580010; PIDN:AAG18952.1; GSPDB:GN00138
C;Genetics:
A;Gene: nthAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 KXXLLXXXGXGLKSXECVRLLXLXX-XAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLX 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 GXIDLEWLRXXXXXXXXXXXLLXXXGXGLKSXECV-RLLXLXXXXAFPVDTNVGRIXVRXGX 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 GWLSLSHLKTLEVDQARWELQALPGVGVKVAACVLNFSDLAMRALVVDTHVDRVARRIGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 VPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXX 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V-----GSGDTTNTYHTLMAMAPASW-----TADDLFELHWLMKRGLGQMLCGAEA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 RAALLDMTGVGPKTADCVLLFAGGAPGVFPVDTHVHRIARRMGIAPAAADHEAVRAALEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 AVPDAA------CGFG------HTAMIQFGR-EYCTARDPACLDDPAACPL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 XYPXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNC----NACPM 198
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A;Title: Genome sequence of Halobacterium species NRC-1. A;Reference number: A84160; MUID:20504483; PMID:11016950 A;Accession: D84198 A;Status: prelimina...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 89.5; DB 2;
Pred. No. 3.9e-06;
8; Mismatches 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 27.6%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CC2272
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Cipecies: Neurospora crassa
Cipacies: Oct-2000
Rischulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, September 2000
A: Reference number: 226053
A: Reference number: 226053
A: Reference number: 2520
A: Seculation of the Protein Nava
A: Molecule type: DNA
A: Residues: 1-572 <SCH>
   A;Accession: F72383
A;Status: preliminary
A;Nolecule type: DNA
A;Rosidues: 1-232 <ARN>
A;Esidues: 1-232 <ARN>
A;Esidues: 1-232 <ARN>
A;Esidues: 1-232 <ARN>
A;Cross-references: GB:AE001718; GB:AE000512; NID:g4980881; PIDN:AAD35467.1; PID:g498
C;Genetics: Strain MSB8
C;Genetics: A;Gene: TM0382
C;Superfamily: Methanococcus jannaschii conserved DNA-(apurinic or apyrimidinic site)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
G86758
NNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) [imported] - Lactococcus li
NNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) [imported] - Lactococcus li
N.Alternate names: endonuclease III
C;Species: Lactococcus lactis subsp. lactis
C;Accession: G86758
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, R.; Weissenbach, J.; l
Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 NLSRLRDLPTHILRERLLKIKGIGKETADAILLYALEKPVFVVDSYTRRLLKRIFNIELN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 PLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----EDVRLYQEFHGLIVEHAKKFCSK-TPKCG 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---CDVKVPDHLKYGLHQLFIRHCQQCF 536
                                                                                                                                                                                                                                                                                                                                                                                                                      75 DLEWLRXXXXXXXXXXLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLX 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 572;
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A;Experimental source: BAC clone B2J23; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                    Length 232;
                                                                                                                                                                                                                                                                                                                                                               68; Indels

    Neurospora crassa

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                                                                                                                                                                                                                                                                                                 Score 76; DB 2;
Pred. No. 0.00047;
                                                                                                                                                                                                                                                                                                                                                            14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein B2J23.160 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 -C-----TKXXPNCNACPM 198
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                                                                                                                                                                                                                                                                                                 11.0%;
ilarity 22.5%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 DY-DEVOKLEMTHYP----
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable endonuclease III - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Oilore 1999 #sequence_revision 03-Dec-1999 #text_change 31-mar-2000
C;Accession: C75459
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Recession: C75459
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: Paserimental source: strain R1
A;Experimental source: strain R1
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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A;Map position: 1
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hypothetical protein TM0382 - Thermotoga maritima (strain MSB8)
c;Species: Thermotoga maritima
c;Species: Thermotoga maritima
c;Species: Thermotoga maritima
c;Accession: F72383
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
A;Cross-references: GB:AP000006; NID:gaisaiss, Figuressian.
A;Experimental source: strain OT3
A;Experimental source: strain OT3
A;Orde: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
A;Gene: PH1498
C;Superfamily: apurinic/apyrimidinic endonuclease III
C;Superfamily: apurinic/apyrimidinic endonuclease III
C;Keywords: 4Fe-45; iron-sulfur protein; metalloprotein
F;195,202,205,211/Binding site: 4Fe-45 cluster (Cys) (covalent) #status predicted
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A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sed
A/Reference number: A72200; MUID:99287316; PMID:10360571
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                                                                                                                                                                                                                                                                                                                                                                                                                         72 GXIDLEWLRX----XXXXXXXKXXLLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 RXGXVPLXPLPXXXQXHXLXXYPXXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFC 186
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                                                                                                                                                                                                                                                                  Length 222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Indels
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                                                                                                                                                                                                                                                               11.8%; Score 82; DB 2; 26.9%; Pred. No. 5.1e-05;
                                                                                                                                                                                                                                                                                                                             10; Mismatches
                                                                                                                                                                                                                                                                                                                          Conservative
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Matches 30; Conserve
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29; Conserv
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Best Local S:
Matches 29,
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C75459
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- Lactococcus lac

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Gaps

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C; Species: Listeria monocytogenes
C; Date: 27-Nov-2001 #text_change 14-Dec-2001
C; Accession: AF1311
C; Daninguez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
C; Acuthors: Kreft, J; Kuhn, M.; Kunst, F.; Kurapkat, G; Maddeno, E.; Maitournam, A.; May Actubras: Kreft, J; Simoss, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Tille: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AF1311
A; Status: prediminary
A; Molecule type: DNA
A; Residues: 1-219 cGLA
A; Rosicules: Strain EGD-e
C; Genetics:
C; Genetics:
A; Experimental source: strain EGD-e
C; Genetics:
A; Experimental source: strain EGD-e
C; Genetics:
A; Superfamily: apurinic/apyrimidinic endonuclease III
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis sa
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable endonuclease III (DNA repair) [imported] - Listeria monocytogenes (strain EGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
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                                                                                             A Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Realdues: 1-1218 <CSTO-
A; Cross-references: CSTO-
A; Cross-references: strain IL1403
A; Experimental source: strain IL1403
C; Generics:
A; Gene: nth
C; Superfamily: apurinic/apyrimidinic endonuclease III
C; Keywords: carbon-oxygen lyase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 KXXLLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXX 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.7%; Score 74; DB 2; Length 218; Best Local Similarity 25.9%; Pred. No. 0.00092; Matches 30; Conservative 9; Mismatches 49; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72; DB 2;
Pred. No. 0.0019;
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10.4%; Score 72; DB 2
Best Local Similarity 25.2%; Pred. No. 0.001
Matches 26; Conservative 8; Mismatches
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Length 259;

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A; Accession: D75275
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-259 <WHI>
A; Residues: 1-259 <WHI>
A; Cross references: GB: AE002073; GB: AE000513; NID: 96460244; PIDN: AAF11977.1; PID: 9646
C; Genetics: Strain R1
C; Genetics: A; Genet
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25.2%;
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Best Local Similarity 25.2%
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypochetical protein At2936490 [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: D84781
S; End. S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUDD: 20083487; PMID: 10617197
A;Rocession: D84781
A;Rolecule type: DNA
A;Residues: 1-1207 <STO>
A;Cross-references: GB:AE002093; NID: 94581149; PIDN: AAD24633.1; GSPDB:GN00139
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 2
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C.; Ma
                                                                                                                     695
                                                                                  A;Map position: 4
A;Introns: 41/3; 70/3; 88/1; 118/1; 321/1; 367/1; 474/1; 504/2; 624/3; 655/2; 667/3; A;Introns: 41/3: 180
C;Superfamily: Arabidopsis thaliana hypothetical protein F28A23.180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gispecies: Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Objecies: Deinococcus radiodurans
C;Accession: D75275
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
K;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
S, Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;R:Rerence number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                            117 VDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYX 176
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                                                                                                                                                                                                                                                                       ch 29.1%; Score 201.5; DB 2;
1 Similarity 49.5%; Pred. No. 2.2e-23;
46; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 XITFGKXXFCTKXXPNCNACPMXXXECXXXXSA 209
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Matches 46; Conserv
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probable DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - Sulfolobus solfat N:Alternate names: endonuclease III; protein c04006 (Species: Sulfolobus solfatraticus C:Species: Sulfolobus solfatraticus C:Species: Guidolobus solfatraticus C:Date: 09-oct-1997 #sequence_revision 24-oct-1997 #text_change 20-Jun-2000 (SAccession: S75373 R:Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, O.Y.; Penny, Mol. Microbiol. 22, 175-191, 1996 A:Title: Organizational characteristics and information content of an archaeal genome A:Reference number: S73076; MUID:97055432; PMID:8899719
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: D84198
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
Jung, K.H.; Alam, M.; Freitess, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Status: nucleic acid sequence not shown; translation not shown
A.Status: nucleic acid sequence not shown; translation not shown
A.Status: nucleic acid sequence not shown; translation not shown
A.Status: 1-236 A.SEN>
A.Status: Strain P2
A.Status: Strain P2
A.Status: A.Status P2
A.Status: A.Status Data Library, September 199
C.Superfamily: apurinic/apyrimidinic endonuclease III
C.Staywords: 4Fe-4S; carbon-oxygen lyase; metalloprotein
F;204,211,214,219/Binding site: 4Fe-4S cluster (Cys) (covalent) **status predicted
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                                                                                                                                                                                                                                                                                                                                              P------LXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXX 177
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                                                                                                Gaps
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                                                                                            Indels
; Score 112.5; DB 2;
; Pred. No. 8.7e-10;
10; Mismatches 49;
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Herzl A.,

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098JQ6 098JQ6;

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Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 KVNLDPETIKEWDVLMVNDSPSRSYDDKETEAKWKKEREIFQTRIDLFINRMHRLQGNRK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --XXXXDXXXXXXXXXERXXFXXRXXXFIXRMXXXQGXRX 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \(\mu\) \(\
                                                                                                                                                                                                                                                 EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO21961; CAA19566.1; --
EMBL; ALI01584; CAB8(123.1; --
                                                                                                          Fartmann B., Granderath K., Dauner I H W., Lemcke K., Mayer K.F.X.;
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                       to the EMBL/GenBank/DDBJ databases
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 112.1 kDa prptein.
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Pred. No. 1.3e-19;
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Pred. No. 9.4;
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Mewes H.W., Mayer K., Schueller C.;
Submitted (FEB-1998) to the EMBL/Ge
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EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/G.
EMBL; ALI62875; CAB85562.1;
Hypothetical protein.
SEQUENCE 1017 AA; 112139 NW; 4:
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Fes_bind.
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28.8%;
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InterPro; IPR003651;
Pfam; PF00730; HhH-GP
                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00478; ENDO3
SMART; SM00525; FES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 917 AA; 1
                                                                                                                                    Neumann S., Mewes H
Submitted (MAR-2000)
                                                                               SEQUENCE FROM N.A. Weichselgartner M.,
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01-0CT-2000
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Local Sim.
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MEDLINE-20003487; PubMed=10617199;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Eujii C.Y., Mason T.M., Bownan C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Grounin L.A., Shen M., VanAken S.B., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Niermun W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

Salzberg S.L., Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-eat cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eldicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
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                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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Pred. No. 9.7e-20;
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53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXAXXFP 90
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
Hypothetical 106.3 kDa protein.
                                                                                                                                                                  PRT; 1207 AA
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InterPro; IPR003651; FeS_bind.
SMART; SM00525; FES; 1...
SEQUENCE 1207 AA, 135916 MW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 402:761-768(1999).
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                                                                                                                                                                  PRELIMINARY;
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STRAIN-CV. COLUMBIA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                          At2g36490 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
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thaliana

Lin X.;

Matches

RESULT

Dauner D.,

QUENCE FROM N.A. Wan,M., Weichselgartner M., Fartmann B., Granderath K., Wan R., Neumann S., Hoheisel J., Jesse T., Helingar-b, V

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049498

RESULT 3

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Length 1017;

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Length

Q9bk13 paramecium Q91v81 arabidopsis Q929e3 listeria in Q9y544 listeria mo Q9p8d6 aspergillus Q23010 caenorhabd1

Q9K9Z1 Q9BK13 Q9LV81 Q929E3 Q8Y544 Q9P8D6

P87638 dengue viru Q8q160 olive leaf

023010 09X0V8 P87638 080L60 09BPZ2 09NUZ1

10 116 116 112 112 4

QBUEES Q9FVN0

thermotoga

09x0v8

Q9k9zl bacillus ha

Q9bp2 homo sapien Q9bp2 homo sapien Q9nuzl homo sapien Q93qk klebsiella Q8dee5 agrobacteri Q6fvn0 lycopersico Q9kry9 vibrio chol Q9zta4 arabidopsis Q9rc22 bacillus sp Q9hhy9 halobacteri Q94dv2 oryza sativ Q17748 caenorhabdi Q9c933 arabidopsis Q9c833 arabidopsis Q9c833 arabidopsis

Q9KRY9 Q9ZTA4 Q9RC22 Q9HHX9 Q94DV2 Q17748 Q9C903

Q9C833 Q91KP0 Q9XCE9

10

O9xce9 streptomyce Q9jy82 neisseria m O26841 methanobact

090wg2 gallus gall 29p9b4 uncultured

PRT; 1309 AA

PRELIMINARY;

ALIGNMENTS

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41.5
41.5
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                                                                                                                                                                                                                                                                                                              09SR66
                                                                                                                                                                                                                                                                                             RESULT 1
Q9SR66
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Q91969 arabidopsis
Q91269 arabidopsis
Q9123 mus musculu
Q94223 mus musculu
Q9422 homo sapien
Q9pt3 ureaplasma
Q9fnq3 arabidopsis
Q95260 arabidopsis
Q95260 arabidopsis
Q95290 arabidopsis
Q93yu0 arabidopsis
Q82w44 pyrobaculum
Q81vm5 arabidopsis
Q82v6 arabidopsis
Q82v6 arabidopsis
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                                                        8, 2002, 19:24:15; Search time 11.1765 Seconds (without alignments) 1659.222 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                            671580
       GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                      671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                         OM protein - protein search, using sw model
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Q49498
Q9LZ69
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Q9Y4C2
Q9PPT3
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Q9PPT3
Q9P3U0
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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: sp_archea:*
: sp_bacteria:*
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length: 200000000
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sp_human:*
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Maximum DB
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CTRAIN=CV. COLUMEIA;

A Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nicmran W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC T22K18 genomic sequence.";
I "Arabidopsis thaliana chromosome III BAC T22K18 genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
I REMBL; AC010927; AAF04422.1;
R InterPro; IPR00365; Endo.3c.
InterPro; IPR00365; Fes\_bind.
R SMART; SM00478; ENDO3C; 1.
SMART; SM00478; ENDO3C; 1.
SMART; SM00525; FES; 1.
C SEQUENCE 1309 AA; 148451 MW; 3B21E4439BAAA673 CRC64; Arabidopsis thaliana (Mouse-ear.cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 497 KVQLDPETSRVWKLLMSSIDCDGVDGSDEEKRKWWEEERNMFHGRANSFIARMRVVQGNR 556 Gaps genomic sequence."; 1 KVXXDXXTXXXWXXLXXXXDXXXXXXXX-----XXERXXFXXXFXXXFIXHXXXQGXR . 6 DB 10; Length 1309; Indels Created)
Last sequence update)
Last annotation update) Score 166.5; DB 10; Pred. No. 3.2e-20; 0; Mismatches 47; 53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90 60.5%; 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19, 722818 10, 22218 Local Similarity 43.4 tes 43, Conservative T22K18.18 protein. SEQUENCE FROM N.A NCBI\_TaxID=3702; Query Match Best Loca Matches DOTA BEAR BEAR DESTANDED TO THE SERVICE OF THE SERV ò g ò

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Q9C9V5 Q93YU0 Q8ZW64 Q8RWM5

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917 1017 541 207 921 11131 373 327 738 765 120 120

46 46 45 44 44

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443 43.5 43.5 43.5 43.5 43.5 43.5 43.5

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RESULT 2

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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                    37 IXXRGXÄXXLXXRIXXXXXXXXXXXXFLXXXVXXXGXIDLEWLRXXXXXXXXXXLLXXXG 96
                                                                                                                                                                                                                                                                                 31 IKERGMNNVLAKRI-----KDFLNRLVREHGNIDLEWLRDVPPDKAKEYLLSIRG 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herzl A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A. Bevan M., Fartmann B., Granderath K., Dauner Bevan M., Weichselgartner M., Fartmann B., Granderath K., Dauner Herzl A., Neumann S., Hoheisel J., Jesse T., Heijnen L., Vos P., Mewes H.W., Mayer K., Schueller C.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                               10;
                                                                                                                                                                                              Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. | Weichselgartner M., Fartmann B., Granderath K., Dauner D., Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021961; CAA17546.1;
EMBL; AL16184; CAB80129.1;
InterPro; IPR002265; Endo_3c.
InterPro; IPR003651; Fed_bind.
                                                                                                                                                         FBDBCE4CD0CC5B81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW; 302B3770ACE1A454 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                       Score 202; DB 10;
Pred. No. 8.1e-26;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                97 XGLKSXECŲRLLXLXXXAFPVDTNVGRIXVRXGXVPLXP 135
                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 201.5; DB 1
Pred. No. 7.8e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Cree 01-JUN-1998 (TrEMBLrel. 06, Last 01-JUN-2001 (TrEMBLrel. 17, Last Hypothetical 106 3 kDa protein. F28A23.180 OR AT4G34060.
                                                                                                                                  119 119
119 AA; 13771 MW;
                                                                                                                                                                                       29.1%;
50.5%;
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SEQUENCE 917 AA, 106310
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Best Local Similarity 49.5
Matches 46; Conservative
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SMART; SM00525; FES; 1.
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                    Asada T.,
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Eukaryota, Viridiplandae, Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnolipphyta; eudicotyledons; core eudicots; Rosidae;
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVRI------KDFLERIVKDHGGIDLE 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 WLRXXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXGXVPLXPLP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Malpighiales; Euphorbiaceae; Euphorbia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarcel R., Glelen J., Van Montagu M., Bancroft I., Mewes H.W., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                              157 XLWPRLCKLXQXTLYELHYXXIIPGKXXFCTKXXPNCNACPMXXXECXXXXSA
                                                                   61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVARDIdopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL162875; CAB85563.1;
InterPro; IPR003265; Endo_3ct
Ffam; PF00730; HhH-GFD, 1
SWART; SW00478; ENDO3c; 1.
Hypothetical protein.
SEQUENCE 555 AA; 62088 MW; AIB44BDDE17FDCIE CRC64;
                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypotherical 62.1 kp protein.
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Pred. No. 1.6e-29;
0; Mismatches 61
                                                                                                                                                                        555 AA
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up. JUN-2002 (TrEMBLrel. 21, Last annotation Putative FPPsynthasel (Fragment).
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PRELIMINARY;

094LX6; Q94LX6

RESULT 3 Q94LX6

Euphorbia tirucalli.

ETFPPS1

ROM N.A.

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Similarity

Query Match Best Local Matches 5

32.9%;

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# GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 8, 2002, 19:24:15; Search time 28.5621 Seconds (without alignments) 1659.222 Million cell updates/sec

US-09-840-743-72 693

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

671580 seqs, 206047115 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0, Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL\_21:\*

1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_mammal:\* sp\_unclassified:\* sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\* sp\_vertebrate:\* sp\_mhc:\* sp\_organelle:\* sp\_phage:\* sp\_plant:\*
sp\_rodent:\* sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		æ				
Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
-	335.5	48.4	1309	10	Q9SR66	O9sr66 arabidopsis
7	228	32.9	555	10	Q9LZ68	
m	202	29.1	119	10	094LX6	
4	201.5	29.1	917	10	049498	
S	139	20.1	1207	10	902360	O9sia6 arabidopsis
9	112.5	16.2	259	16	Q9RRQ0	
7	89.5	12.9	236	17	P95945	P95945 sulfolobus
80	89.5	12.9	265	17	Q9HS56	
σ	87.5	12.6	223	17	Q9P9L7	_
10	86.5	12.5	241	16	Q9A623	09a623 caulobacter
11	98	12.4	222	17	9M0A60	-
12	84	12.1	225	17	овитне	
13	83.5	12.0	233	17	026858	026858 methanobact
14	83	12.0	224	17	Q971F2	
15	82	11.8	222	17	059167	_
16	78.5	11.3	338	16	Q9RVU4	•

Q9wy13 thermotoga Q9rg15 thermoanaer Q9ff16 neuroSpora Q9cgm5 lactococcus Q9cgm5 lactococcus Q9cha8 methanosarc Q9zab4 listeria in Q8y608 listeria mo Q8tyu8 methanopyru Q9z1p6 helicobacte Q25307 helicobacte Q5663 aquifex aeo Q9k76 bacillus ha Q9yfv0 aeropyrum p Q99u37 staphylococ Q9k56 methanopyru G9tys methanopyru G9tys methanopyru G9tys methanopyru Q9tys thermoplasm Q9lcrl paenibacill Q9vih0 drosophila	
16 09WYL3 16 08R857 16 09CGMS 17 08THAB 16 092AB4 16 092AB4 16 092AB4 16 092AB4 16 095AB7 17 091AB7 17 099U37 2 09EUT1 17 0898B1 17 0898B1 17 087AM6 17 087AM6 18 097AM7 2 09EUR1 2 09EUR1 2 09EUR1 2 09EUR1 2 09EUR1 2 09EUR1 2 09EUR1	16 09CBJO 16 097FM4 16 097CEO 5 09M592 16 097L73 16 098GU1
	297 292 209 1072 211 238
	8888888 200887.
7 4 4 7 4 4 7 4 4 7 4 4 7 4 4 7 4 4 7 4 4 7 4 4 7 4 4 7 4 4 7 4 4 7 4	62 61.5 61 61 60.5
11188 1188 1188 1188 1188 1188 1188 11	44444

## ALIGNMENTS

RESI	RESULT 1	
200	OSSR66 PRELIMINARY; PRT; 1309 AA. OSSR66:	
DI	01-MAY-2000 (TrEMBLrel. 13,	
E E	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
E	T22K18.18 protein.	
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S Z	NCB1_10A1D=3/02;	
RP	SEQUENCE FROM N.A.	
RC		
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DR	Pfam; PF00730; H	
DR	SMART; SM00478;	
E.	SMART; SM00525; FES; 1.	
SO	SEQUENCE 1309 AA; 148451 MW; 3B21E4439BA4A673 CRC64;	
õ	h 48.4%;	
æ	Similarity 47.4%; Pred. No. 3.1e-47;	
Ψç	0	rn
ογ	37 IXXRGXXXXXXXXXXXXXXXXXXXXXX 96	
q	832 IIKRGMNNMLAERIKAFLNRLVKKHGSIDLEWLRDVPPDKAKEYLLSING	881

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97 XGLKSXECVRLLXXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQK 156

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OBRWMS

OBRAMS

TO 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

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Search completed: November 8, 2002, 19:28:34 Job time : 14.1765 secs

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SEQUENCE FROM N.A.

Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
Yamada K., Banh J., Banno F., Chang C., Toriumi M., Wu H.C.,
Yamanura Y., Yu G., Wu S., Bowser L., Carninci P., Chen H., Cheuk R.,
Hayashizaki Y., Ishida J., Jones T., Ramiya A., Rarlin-Neumann G.,
Rawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
Ecker J.R., Theologis A.;
"Full Length conno of gene At1967890 (GI:15220577).";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.6%; Score 43; DB 17; Length 120; 38.9%; Pred. No. 12; Live 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00086; PAC; 1.
TIGREAMS; TIGR00229; sensory_box; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
ATP-binding; Hypothetical protein; Transferase.
SEQUENCE 765 AA; 85149 MW; 6651738FB4E347D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL. AE009849; AAL63838.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 120 AA; 13398 MW; 34DP06D06226AD5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein PAE1954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 78;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43.5;
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000719; Euk_Pkinase.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS_domain.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00785; PAC; 1.
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STRAIN-IM2 / ATCC 51768 / DSM 7523;
PubMed-11792869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 RGNLIQSPFGVFLC-NDDKSSSKA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermoproteaceae; Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 FXXWKGSVVDSVXGVFLT 71
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Best Local Similarity 38.5.
7; Conservative
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF00989; PAS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=13773;
                                                                    NCBI_TaxID=3702
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White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,

A Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A Chung M.K., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

A Lin S.X., Liu S.X., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Naywen M., Nlerman W.C., Osborne B.I.,

Rad G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Whith Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Whiterback T., van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Surosids II; Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Hypothetical protein; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 408:816-820(2000).
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. EMBL; AC012563; AAG52018.1; -. HSSP; P12931: 1FWX
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 85.1 kDa protein.
ATIG67890.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO, IPRO00719; EUK_pkinase.
INTERPRO; IPRO01619; PAC_
INTERPRO; IPRO000014; PAS_domain.
INTERPRO; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rickrams; rick00229; sensory_box; 1
                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
MEDLINE-21016719; Pubmed-11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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ProDom; PD000001; Euk_pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 KGSVVDSVXGVFLTQNXDXXSSXA 81
Hypothetical 82.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00086; PAC; I.
SMART; SM00091; PAS; I.
SMART; SM00220; S_TKC; I.
SMART; SM00219; TYTKC; I.
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Pfam; PF00989; PAS; 1
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                                                                                                                                  NCBI_TaxID=3702;
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Query Match

Matches

Db δy

093YU0

RESULT 13
093YU0
093YU
093YU
AC 093YU
DT 01-DE
DT 01-DE
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Gaps

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Gaps

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RESULT 9

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SEQUENCE FROM N.A.
Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Bancroft I., Mowes H.W., Mayer K.F.X., Schueller C.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thallana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                DB 3; Length 1141; 99;
                                                                                                                                                                                                                                    10; Indels
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL360054; CAB96001.1; -.
InterPror; IPR001394; UCH-2.
Pfam; PF00443; UCH-1; 1.
PROSITE; PS00973; UCH-2.1; 1.
PROSITE; PS00973; UCH-2.1; 1.
PROSITE; PS00973; UCH-2.2; 1.
                                                                                                                                                              1499E32DB6CB26CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; ALO49638; CAB40936.1; -.
EMBL; ALO45533; CAB78238.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing project;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 327 AA; 35845 MW; B2BB47DF4A83E635 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 35.8 kDa protein.
F16013.20 OR AT4611950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                  Score 44; DB 3; Pred. No. 99; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     327 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.8%; Score 43.5; 41.7%; Pred. No. 31;
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                                                                                                                                                                                                                                                                                                            882 KQTLYDALDGVFETVNIDMGSETA 905
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                                                                                                                                                              1141 AA; 130296 MW;
                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                        58 KGSVVDSVXGVFLTQNXDXXSSXA
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(TrEMBLrel. 17, I
(TrEMBLrel. 21, I
                                                                                                                                                                                                  16.0%;
41.7%;
                                                                                                                                                                                                  Query Match 16.0
Best Local Similarity 41.7
Matches 10; Conservative
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nes 10; Conserv
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01-JUN-2001 (
01-JUN-2002 (
                                                                                                                                               Hydrolase.
                                                                                                                                                                  SEQUENCE
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Q9C9V5;
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Q9C9V5
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       δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viidiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of Arabidopsis thaliana chromosome 5. II. Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned P1 clones.";
DNA Res. 4:291-300(1997).
BMBL; AB006696; BAB10374.1. -.
SEQUENCE 373 AA; 41666 MW; 48B8C3396A9832D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-COLUMBIA;
MEDLINE-98069011; PubMed-9405937;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=972H-;
Saunders D., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ر.
د
                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                    DB 16; Length 1131;
     "The complete sequence of the mucosal pathogen Ureaplasma
                                  Nature 407:757-762(2000).

EMBL; AE002154; AAF30970.1; -.

InterPro; IPR001547; GH_5.

InterPro; IPR00914; SBP_bac_5.

Pfam; PF00496; SBP_bac_5, 2.

PROSTE; PS00659; GIYCOSYL HYDROL_F5; UNKNOWN_1.

Hypothetical protein; Complete proteome.

SEQUENCE 1131 AA; 130078 MW; C45DBBF61E18690B CRC64;
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                                                                                                                                                                                                                                        Indels
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Schlzosaccharomyces pombe (Fission yeast).
Bukaryota; Fungl: Ascomycota; Schlzosaccharomycetes;
Schlzosaccharomycetales; Schlzosaccharomycetaceae;
Schlzosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Ubiquitin carboxyl-terminal hydrolase.
                                                                                                                                                                                                                                      7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
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Pred. No. 24;
1; Mismatches
                                                                                                                                                                                                  Score 45; DB 1
Pred. No. 66;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 WKGSVVDSVX----GVFLTQ 72
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47.6%;
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50.0%;
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                                                                                                                                                                                                                                                                                                          744 FDKYAGSTYDSALGLFLT 761
                                                                                                                                                                                                                                                                          54 FXXWKGSVVDSVXGVFLT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
                                                                                                                                                                                                                   Local Similarity 50.0 nes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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Best Local &
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SEQUENCE
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Arakawa T., Hara A., Shibata K., Yoshino M., Itch M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsud H.A., Ashburner M., Batalov S., Casavant T.,
Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Balaka J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Rownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P.,
Alayashizah R., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Hayashizah A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizahi Y., Hayashizah Y., Kawaji H., Kohtsuki S.,
Hayashizahi Y., Hayashizahi Y., Rawaji H., Kohtsuki S.,
Hayashizahi Y., Rawai Y., Kawaji H., Kohtsuki S.,
Hayashizahi Y., Hayasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metaria; Crordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL: Z48638; CAA88567.1; -
WormPep; ZK892.3; CE01726.
                                                                               01-JAN-1999 (TrEMBLrel. 09, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 61.0 kDa protein ZK892.3 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 AA; 61045 MW; A7A1D7EDB140AC6F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 RTFSNWANARILVVFVAFITRRWDTASYVCAAISALIFP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001569; Actbind_actnin.
InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
PROSITE; PS00019; ACTININ_1; UNKNOWN_1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 RXFXXWKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
                                  541 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 13;
4; Mismatches
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Matches 11; Conservative
                               PRELIMINARY;
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                                                                                                                                                                                                                        Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 541 AA; 6
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09D22
AC 09D22
AC 09D22
AC 09D22
AC 09D22
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"Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=SEROVAR 3;
MEDLINE-20500219; PubMed-11048724;
Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
Cassell G.H.;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                           DB 11; Length 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 921;
                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO18281; BAA34458.1; -.
EMBL; BC000609; AAH00609.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03D39FDF90561F74 CRC64;
EMBL; AK020704; BAB32184.1; -.
MGD; MGI:1924824; A230020K05Rik.
SEQUENCE 207 AA; 22411 MW; 558A70EC798BB4C9 CRC64;
                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                           6.7;
                                                                                                                                                                                                                                                                                     921 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                Mismatches
                                                                           Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99087487; PubMed=9872452;
                                                                                                                                                                                      165 RVLFAFPGNLVTSVAGVYFTDN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            921 AA; 102139 MW;
                                                                                                                                               52 RXFXXWKGSVVDSVXGVFLTQN 73
                                                                         16.7%;
40.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasmataceae; Ureaplasma.
NCBI_TaxID=134821;
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                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE OF 1-919 FROM N.A.
                                                                                                              9; Conservative
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                            KIAA0738 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                    Q9Y4C2; Q9BW63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=BRAIN
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Query Match
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Matches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. COLUMBIA;
MEDLINE-20083487; Pubbed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAens S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiphantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KVXXDXXTXXXWXXL-----XXXXDXXXXXXXXXXERXXFXXXXXXXXIXRMXXXQGXR 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F28A23.180 OR AT4G34060.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Herzl A., Neumann S., Hoheisel J., Jesse T., Heijnen L., Vos P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 163.5; DB 10; Length 1207; Pred. No. 9.7e-20;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 106.3 kDa protein.
                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
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                                                                                                                                                                                       1207
                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.5%;
                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lin X.;
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                          At2g36490 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 KVNLDPETIKEWDVLAVNDSPSRSYDDKETEAKWKKEREIFQTRIDLFINRMHRLQGNRK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                    Herzl A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KVXXDXXTXXXWXXL-----XXXXDXXXXXXXXXXXERXXFXXRXXXFIXRMXXXQGXRX
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Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R.,
De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
Villarcel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.
Rudd S., Lemcke K., Mayer K.R.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  917;
                                                                                                                    Dauner D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; Al162875; CABS5562.1; -.
Hypothetical protein.
SEQUENCE 1017 AA; 112139 WW; 4F7C313A891EC83F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                               SEQUENCE FROM N.A.

FU Arabidopsis sequencing project;

ED Arabidopsis sequencing project;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL021961; CAA17566.1; -.

EMBL; AL16184; CAB80123.1; -.

InterPro; IPR002565; Endo.3c.

InterPro; IPR00265; Fes_blnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                  SEQUENCE FROM N.A. Weichselgartner M., Fartmann B., Granderath K., Dauner I Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
Mewes H.W., Mayer K., Schueller C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l protein.
917 AA; 106310 MW; 302B3770ACE1A454 CRC64;
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-077-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 112.1 kba protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.0%; Score 49.5; DB 10;
11arity 28.8%; Pred. No. 9.4;
Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 9%; Score 162; DB 10;
ilarity 43.9%; Pred. No. 1.3e-19;
Conservative 0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FKOWKGSVVDSVVGVFLTONTTDYLSSNAFMSVAAKFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1017
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00730; HhH-GPD; I. SMART; SM00478; ENDO3c; I. SMART; SM00525; FES; I. Hypothetical protein. SEQUENCE 917 AA; 106310 P
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hes 43; Conserv
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nes 17; Conserv
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09k9z1 bacillus ha

Q9bk13 paramecium

0929e3 listeria in 08y544 listeria mo

Q9p8d6 aspergillus Q23010 caenorhabdi

Q9x0v8 thermotoga P87638 dengue viru Q8q160 olive leaf

homo sapien homo sapien

09bpz2 Q9nuz1

0933K8 Klebsiella 08uee5 agrobacteri 09fv00 lycopersico 09kry9 vibrio chol 09zta4 arabidopsis 09rc22 bacillus sp

Q9jy82 neisseria m O26841 methanobact Q90wg2 gallus gall Q9p9b4 uncultured

5

Q9c903 arabidopsis Q9c833 arabidopsis Q91kp0 dengue viru Q9xce9 streptomyce

O9hhx9 halobacteri O94dv2 oryza sativ O17748 caenorhabdi

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STRAIN-CV. COLUMBIA;

Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,

Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,

Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,

Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,

Bowman C.L., White O. Nierman W.C., Fraser C.M.;

"Arabidopsis thaliana chromosome III BAC T22K18 genomic sequence.";

L. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AC010927; AAF04422.1;

R. InterPro: IPR003265; Endo.3c.

InterPro: IPR003265; Endo.3c.

InterPro: IPR003651; Fes_bind.

R. Pfan: PF00730; HH-GPD; 1.

R. SMART; SM00478; ENDO32; 1.

R. SMART; SM00525; FES; 1.

O SEQUENCE 1309 AA; 148451 MW; 3B21E4439BA4A673 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497 KVQLDPETSRVWKLLMSSIDCDGVDGSDEEKRKWWEEERNMFHGRANSFIARMRVVQGNR 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 1309;
                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.5%; Score 166.5; DB 1
43.4%; Pred. No. 3.2e-20;
ive 0; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                         PRT; 1309 AA
                                                                                                                                                                                                                                                                                                         ALIGNMENTS
         Q9BK13
Q9LV81
Q929E3
Q8Y544
                                                Q9P8D6
Q23010
Q9X0V8
P87638
Q8QL60
Q9BPZ2
Q9NUZ1
Q93GK8
                                                                                                                                      Q9FVNO
Q9KRY9
Q9ZTA4
Q9RC22
Q9HX29
Q94DV2
Q17748
Q9C903
Q9C903
Q9C833
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Q26841
Q90WG2
Q9P9B4
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                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
294
306
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049498 arabidopsis
091z69 arabidopsis
000617 caenorhabdi
090223 mus musculu
0994c2 homo sapien
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Q9fnq3 arabidopsis
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09c9v5 arabidopsis
093yu0 arabidopsis
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Q8rwm5 arabidopsis
Q9c9e0 arabidopsis
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                                                                                                                                                                                                                                                                                 Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.; "Complete genome sequence of an aerobic thermoacidophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
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                                                                                                                Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 ----REYW-----IELNDLMVQFGQ-DICRPLGPRHEECPI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endonuclease; Complete proteome.
SEQUENCE 233 AA; 27012 MW; 10F6163AAE98395B CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative endonuclease III.
01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.0%;
26.9%;
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PubMed=11572479;
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Sulfolobus tokodaii
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NCBI_TaxID=111955;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                        NCBI_TaxID=187420;
                                                         Endonuclease III.
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01-DEC-2001 (
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Kudoh Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H., "Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
EMBL, APO00006; BAA30606.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 LXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXX 151
                                                                                                                                                                                                                                                                                                                                                                                                                     '18;' Gaps
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                                                                                                                                                                                                                                                                                                                                                             Length 224;
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Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res, 8:123-140(2001).
EMBL; AP000986; BAB66468.1;
InterPro; IPR003265; EndoIII_FCL.
InterPro; IPR003265; EndoIII_FCL.
InterPro; IPR003283; HHHL].
Ffam; PF00730; HHH-GPD; 1.
SMART; SM00278; HHH1; 1.
PROSITE; SS00764; ENDONUCLEASE_III_1; UNKNOWN_1.
PGANGIOSE 224 AA; 25629 MW; E2BE3A0762135550 CRC64;
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Best Local Similarity 26.9%; Pred. No. 2.4e-Up;
Best Local Similarity 26.9%; Pred. No. 2.4e-Up;
Matches 29; Conservative 10; Mismatches 51; Indels
Matches 29; Conservative 10; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 XXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD096F91C969DF0C CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
222AA long hypothetical endonuclease III.
PH1498.
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PROSITE; PS01155; ENDONUCLEASE_III_2; UNKNOWN_1.
Endonuclease; Complete proteome.
SEQUENCE 222 AA; 25553 MM; DD096F91C969DF0C (
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InterPro; IPR004036; EndoIII_HhH.
InterPro; IPR003565; Endo_3c.
InterPro; IPR003561; FeS_bind.
InterPro; IPR003583; HHH_1.
Ffam; PF00730; HhH-GPD; 1.
SMART; SM00578; FES, 1.
SMART; SM00578; HHH; 1.
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Matches 27; Conserv
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"Pyrococcus abyssi genome sequence: insights into archaeal chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                             118 LIKLPGIGRKCANIVLAYGFGIPAIPVDTHVYRISRRLGLAPWDASPEEVEERL----- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyrococcus furiosus.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
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Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AG010230; AAL81353.1; -
Complete proteome.
SEQUENCE 225 AA; 26157 MW; DA48762AC33EE4AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --EILKTLIP----VEEWIY-VNHAMVDHGK-SICRPIKPKCELCPL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 -----KELIPR-----EBWIY-VNHAMVDHGK-SVCRPIKPRCDECPL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                   Structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AJ3482B5; CAB49586.1; --
HSSP; P20625; 2ABK.
                                                                                                                                                                                                                                       PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
PROSITE; PS01155; ENDONUCLEASE_III_2; UNKNOWN_1.
Endonuclease; Complete proteome.
SEQUENCE 222 AA; 25541 MW; 27F0B5FC838C0DC6 CRC64;
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                                                                                                                                                                                                                                                                                                                          / Match 12.4%; Score 86; DB Local Similarity 26.9%; Pred. No. 5.1e les 29; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seque
01-JUN-2002 (TrEMBLrel. 21, Last annoi
Glycosylase putative, mutY-nth family
PF1229.
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                                                                               InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR004036; EndoIII_HhH.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003361; HHH_1.
Endo, IPR00350; HHH_1.
Ffam; PF00730; HHH-GPD; 1.
SMART; SM00278; ENS; 1.
SMART; SM00278; HHH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 25.9%
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                            Query Match
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026858
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEATAIN-ATCC 19089 / CB15;

MEDLINE-21173698; PubMed-11259647;

MEDLINE-21173698; PubMed-11259647;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Beisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

Potocka I., Nelson W.J., Durkin A.S., Gwinn M.L., Haft D.H.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

"Complete genome Sequence of Caulobacter crescentus.";

REMBL; AE005897; AAKZ4243.1; -.

RIGR; CC2272; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 VPLXPLPXXXQXHXLXXXPXXXXXXQKXLMPRLCKLXQXTLYELHYXXITFGKXXFCTKXX 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 GXIDLEWLRXXXXXXXXXXXXLXXXGXGLKSXECV-RLLXLXXXAFPVDTNVGRIXVRXGX 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 V-----GSGDTTNTYHTLMAMAPASW-----TADDLFELHWLMKRGLGQMLCGAEA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyrococcus abyssi.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
162 EKYDEISRW-FMERLPRDKYLDFHLKLIQFGR-DVCRARNPKCGQCPI-GAKCPSFKSA 217
                                                                                                                                                                                                       Caulobacter crescentus.
Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.5%; Score 86.5; DB 16; Length 241; 24.2%; Pred. No. 4.5e-06; ive 9; Mismatches 73; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 AA; 26421 MW; EB43FBA976736F1C CRC64;
                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Endonuclease III family protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 AA
                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; CC2272; -...
InterPro; IRR003265; Endo_3c.
InterPro; IPR003651; FeS_bind.
Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENO3c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY 2000 (TrEMBLrel. 13, 01-MAY 2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, Endonuclease III (NTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.55
Best Local Similarity 24.27
Matches 31; Conservative
                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                       NCBI_TaxID=155892;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 PNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 PKCGACPV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrococcus,
NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTH OR PAB0459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-ORSAY;
Heilig R.;
                                                                                                                                                                                                                                          Caulobacter
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Q9V0W6
                                                   RESULT 10
                                                                      Q9A623
Dp.
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225 AA

18;

233 AA

Length 225

Gaps

Indels

Length 222;

DB 17; 5.1e-06;

us-09-840-743-72.rspt

5,

Gaps

23;

Length 265; Indels

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88 KXXLLXXXGXGLKSXECVRLLXLXX-XAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLX 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of a thermostable DNA glycosylase specific for U/G and T/G mismatches from the hyperthermophilic archaeon Pyrobaculum aerophilum.";
                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
Putative DNA glycosylase (DNA-(apurinic or apyrimidinic site) lyase)
(endonuclease III, PaNKh)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                            RAALLDMTGVGPKTADCVLLFAGGAPGVFPVDTHVHRIARRMGIAPAAADHEAVRAALEA
                                                                                                                                                                                                                 147 XYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNC----NACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILE-20138151; PubMed=10671447;
Yang H., Fitz-Gibbon S., Marcotte E.M., Tai J.H., Hyman E.C.,
Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%; Score 87.5; DB 17; Length 223; 26.9%; Pred. No. 2.8e-06;
                       CEFB1A2A1DB9735E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyase, Endonuclease, Complete proteome.
SEOUENCE 223 AA; 25323 MW; 8A8445E9462167E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
                                                      Score 89.5; DB 17;
Pred. No. 1.6e-06;
                                                                                         53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00764; ENDONUCLEASE_III_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
Proc. AF222334; AAF37269.1; -.
EMBL; AE009791; AAL63095.1; -.
                                                                                                                                                                                                                                                                                                                       223 AA.
                                                                                         8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                         Created)
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STRAIN-IM2 / ATCC 51768 / DSM 7523;
PubMed-11792869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, 220625; 2ABK.
InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003551; FeS_bind.
InterPro; IPR003583; HHH_1.
Ffam; PF00730; HHH-GPD; 1.
SWART; SW00478; ENDO3c; 1.
SWART; SW006225; FES; 1.
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 182:1272-1279(2000).
                       27481 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermoproteaceae; Pyrobaculum
                                                        12.9%;
27.6%;
                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Conservative
                                                                                         Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                         265 AA;
                                                        Query Match
Best Local Similarity
       Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miller J.H.;
                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                     Q9P9L7
                                                                                                                                                              145
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         SOW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20504483; PubMed=11016950;
NA MEDLINE-20504483; PubMed=11016950;
NA NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Ng W.V., Kennedy S.P., Mahairas G.G., Estquist B., Pan M.,
Ng Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Ng Swartzell S., Weil D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Ng Alan M.J., Weller K., Cruz R., Danson M.J., Hough D.W.,
Ng Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Ng Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Ng Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ng Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.,
Ng Genome sequence of Halobacterium species NRC-1.";
Ng Proc. Natl. Acad. Sci. U.S. A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                             4
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Frauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.,
"The complete genome of the crenarcheon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
EMBL: AR80655; ZABK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 LLXXXGXGLKSXECVRLL---XLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXX 147
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.9%; Score 89.5; DB 17; Length 236; Best Local Similarity 27.5%; Pred. No. 1.4e-06; Matches 30; Conservative 9; Mismatches 49; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 YPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 YSLISSTLKELF-----SAYDLLHHHMLIAHGRQT-CKARKPLCNSC 214
                                                                                                                                                                                     InterPro; IPR003565; EndoIII_FCL.
InterPro; IPR003565; Endo_3c_
InterPro; IPR003565; Endo_3c_
InterPro; IPR003565; Endo_3c_
InterPro; IPR003565; Fec_bind.
InterPro; IPR003581; HHH.1.
R PRMRT; SM00478; ENDO3c; 1.
SMART; SM00278; HHH1; 1.
R PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
R PROSITE; Lyase; Complete protecome.
SEQUENCE 236 AA; 26843 MM; 6FF5CADB280ECCD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halobacterium sp. (strain NRC-1).
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 AA.
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InterPro: IPR003651; FeS bind.
InterPro: IPR003691; HHL_1.
InterPro: IPR000408; Reg_chr_condens.
Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
SMART; SM00278; FES; 1.
SMART; SM00278; HhH1; 1.
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5

Gaps

Indels

m

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SEQUENCE FROM N.A.

STRAIN=CV. COLUMBIA;

MEDLINE=20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

Salzberg S.L., Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                917 VP-----YELHYQMITFGK-VFCTKSK 942
                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 XGXIDLEWLRXXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXCX 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 VPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXX 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        846 EKTRSTMDTVDWKAIRAADVKEVAETIKSRGMNHKLAERIQYLTLNMKIMOGFLDRLVND 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.1%; Score 139; DB 10; Length 1207; 25.1%; Pred. No. 3.4e-14; ive 0; Mismatches 65; Indels 84,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDB6C9EE94DDF67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                  A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135916 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2000 (TrEMBLrel. 13, Cr
01-MAR-2000 (TrEMBLrel. 13, La.
01-MAR-2002 (TrEMBLrel. 20, Las
Endonuclease III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AC006919; AAD24633.1; -. InterPro; IPR003651; Fes_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 PNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            943 PNCNACPM-KGECRHFASA 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.19
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402:761-768(1999).
                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          906 HGSIDLEWLR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1207 AA;
                                                                                                             At2g36490 protein.
AT2G36490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM(
SEQUENCE
                                90LS60
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RESULT 5
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ID Q9
AC Q9
DJ Q1
DJ Q1
DJ G1
CG BE
CG BE
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Sensen C.W., Klenk H.-P., Singh R.K., Allard G., Chan C.C.-Y.,
Liu Q.Y., Penny S.L., Young F., Schenk M.E., Gaasterland T.,
Doolittle W.F., Ragan M.A., Charlebois R.L.,
"Organizational characteristics and information content of an archaeal
genome: 156 kb of sequence from Sulfolobus solfataricus P2.";
Mol. Microbiol. 22:175-191(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 GXIDLEWLRXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-----LXPLPXXXQXHXLXXYPXXXXQKXLWPRLCKLXQXTLYELHYXX 177
                                                              MEDLINE=20036896; PubMed=10567266; White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.2%; Score 112.5; DB 16; Length 259; 25.2%; Pred. No. 2.1e-10; Live 10; Mismatches 49; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=21332296; Pubmed=11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
                                                                                                                                                                                                  "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Endonuclease III (DNA endonuclease III, probable) (NTH-1)
                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00764; EMDONUCLEASE_III_1; 1.
Endonuclease; Complete proteome.
SEQUENCE 259 AA; 28946 MW; AA07354719093547 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 AA
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STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-97055432; Pubmed-8899719;
                                                                                                                                                                                                                                                                                      InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003651; Fes_bind.
Pfam; PF00730; HHH-GFD; 1.
SMART; SM00478; ENDO3c; 1.
                                                                                                                                                                                                                                 Science 286:1571-1577(1999).
EMBL; AE002073; AAF11977.1; -.
TIGR; DR2438; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 ITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 LSHGR-QVCTWTRPKCGKC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTH-1 OR SSO0116 OR C04006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfolobus solfataricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2287;
NCBI_TaxID=1299;
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                                                                                                                                                                                          Fraser C.M.;
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P95945
δλ
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049498;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
         930
                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 WLRXXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXGXVPLXPLP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euphorbia tirucalli.
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Euphorbia.
NCBL_TaxID=142860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 DSIDYEAIRRASISEISEAIKERGMNNMLAVRI------KDFLERIVKDHGGIDLE 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarcol R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W. Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.9%; Score 228; DB 10; Length 555; 44.5%; Pred. No. 1.6e-29;
                              157 XLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXECXXXXSA
                                            -----ELYELHYHMITFGK-VFCTKVKPNCNACPM-KAECRHYSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUBMITTED (WAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL162875; CAB85563.1; -InterPro; IPR00255; EMDC_3C.
Fran, PF00730, HRH-GPD; 1.
SMART; SM00478; ENDO3C; 1.
Hypothetical protein.
SEQUENCE 555 AA; 62088 MW; AlB44BDDE17FDC1E CRC64;
                                                                                                                               01-ocr-2000 (TrEMBLrel. 15, Created)
01-ocr-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 62.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Conservative
                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 XXXQXHXL 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              546 ESLOLHLL 553
                                                                                                                                                                                                                        eurosids II; Bra:
NCBI_TaxID=3702;
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01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                            09LZ68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       094LX6
                                                     931
                                                                                    RESULT 2
Q9LZ68
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Q94LX6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Varidiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>`</u>
                                                                                                                                                                                                                                                                                                                                                                37 IXXRGXXXXLXXXXXXXXXXXXXXXXVXXXXXXXIDLEWLRXXXXXXXXXXLLXXXG
                                                                                                                                                                                                                                                                                                                                                                                        10;
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Bevan M., Weichselgartner M., Fartmann B., Granderath K., Dau
Herzl A., Neumann S., Hoheisel J., Jesse T., Heljnen L., Vos
Mewes H.W., Mayer K., Schueller C.;
                                                                                                                                                                                                                                                          Length 119;
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Asada T., Fukusaki E., Kobayashi A., Sando T.;
"Prenyltransferase of Euphorbia tirucalli.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO51105; BAB47587.1;
InterPro; IRR03265; Endo_3c.
Pfam; PF00730; HHH-GPD; 1.
                                                                                                                                                                                                                                                                                                             Indels
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EU Arabidopsis sequencing project;
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021961; CAA17566.1; -.
EMBL; AL05184; CAB0123.1; -.
InterPro; IPR002565; Endo_3c.
InterPro; IPR003651; PeS_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weichselgartner M., Fartmann B., Granderath K., Dauner Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 917 AA; 106310 MW; 302B3770ACE1A454 CRC64;
                                                                                                                                                                                                        FBDBCE4CD0CC5B81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 106.3 kDa protein.
F28A23.180 OR AT4G34060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 8.1e-26;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXP 135
                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.1%; Score 201.5; DB 1
49.5%; Pred. No. 7.8e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    662 MITFGK-VFCTKTIPNCNACPM-KSECKYFASA 692
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                                                                                                                                                                                                                                                        Score 202;
                                                                                                                                                                                                          119 AA; 13771 MW;
                                                                                                                                                                                                                                                        29.1%; 50.5%;
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SMART; SM00478; ENDO3C; 1.
SMART; SM00525; FES; 1.
                                                                                                                                                                                                                                                                                     Best Local Similarity 50.5
Matches 50; Conservative
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Matches 46; Conservative
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                                                                                                                                                                                  119
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08tyu8 methanopyru 092t20 rhizobium m 09z1p6 helicobacte 025307 helicobacte

Q9cgm5 lactococcus Q8tha8 methanosarc Q92ab4 listeria in Q8y608 listeria mo

Q9hfi6 neurospora

0321p6 helicobacte 025307 helicobacte 025307 helicobacte 06636 aquifex aeo 09k76 bacillus ha 09yfv0 aeropyrum p 09yfv0 aeropyrum p 09utl staphylococ 08tk57 methanosarc 08tk57 methanosarc 08tk57 methanosarc 08twm6 methanopyru 097aj2 thermoplasm

O9rxml deinococcus Q9cbj0 mycobacteri Q97fm4 clostridium Q97qe0 streptococc Q9w592 drosophila Q97173 clostridium Q98gul rhizobium l

091crl paenibacill 09vih0 drosophila

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STRAIN-CV. COLUMBIA;

Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,

A Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Barnstead M.E.,

Renning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,

A Arabidopsis thaliana chromosome III BAC T22K18 genomic sequence.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

BEL; AC010927; AAF04422.1;

TherPro; IRR00325; Endo_3c.

RICHERPO; IRR00325; Endo_3c.

RICHERPO; IRR00335; ESS_bind.

SRART; SM00478; ENDO3c; 1.

SMART; SM00478; ENDO3c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IXXRGXXXXXLXXRIXXXXXXXXXXXXXFLXXXVXXXGXIDLEWLRXXXXXXXXXXXXX 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1309 AA; 148451 MW; 3B21E4439BA4A673 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
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09CBJ0
097FM4
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Q92T20
Q92LP6
025307
066636
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Q99U37
Q9EUT1
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Q28581
Q8TVM6
Q97AJ2
                                                                          Q92AB4
Q8Y608
                                              Q9CGM5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T22K18.18 protein.
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Q91268 arabidopsis
Q94186 euphorbia t
Q9498 arabidopsis
Q9rrg deinococcus
P95945 sulfolobus
Q9hs56 halobacteri
Q9p917 pyrobaculum
Q9a623 aculobacteri
Q9V0W6 pyrococcus
Q9V0W6 pyrococcus
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                                                                                                   2002, 19:24:15 ; Search time 28.5621 Seconds (without alignments) 1659.222 Million cell updates/sec
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                                                                                                                                                                                                Description
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09rvu4
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              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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693
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deinococcus sulfolobus pyrococcus

Score

Result . 9

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Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens (Strain CS8, Dup C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: 11-3n-2002 #text_change 11-3n-2002 (Species: 11-3n-2002 #text_change 11-3n-2002 (Species: 11-3n-2002 Species: 11-3n-2009 Species: 11-3n-2009 Species: 11-3n-2009 Species: Agrobacterium to Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wooderage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl. Science 294, 2317-2332, 2001 A; Aththors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                       Nature 399, 323-329, 1999
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: H72278
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-832 <ARN>
A;Residues: 1-832 <ARN>
A;Cross-references: GB:AE001779; GB:AE000512; NID:g4981777; PIDN:AAD36306.1; PID:g498
C;Genetics:
                                                                                           Tipha mannosidase-related protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H72278
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicgartett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; PMID:11743193

A;Accession: AE2799
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-432 <KUR>
A; Cross-references: GB: AE008688; PIDN: AAL42811.1; PID: 917740257; GSPDB: GN00186
A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.3%; Score 42; DB 2; Length 432;
.larity 31.0%; Pred. No. 38;
Conservative 6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB;
Pred. No. 52;
1; Mismatches
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A;Map position: circular chromosome
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Best Local Similarity 64.3%;
Matches 9; Conservative
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160 WKGSDGTAVQGVFL 173
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Job time: 8.88235 secs
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                              hypothetical protein homolog lin2334 [imported] - Listeria innocua (strain Clip11262)
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A;Molecule type: DNA
A;Residues: 1-565 <GRE>
A;Coss-references: EMBL:U64853; PIDN:AAB04976.1; GSPDB:GN00023; CESP:K11G9.1
A;Experimental source: strain Bristol N2; clone K11G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein K11G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
                                                                                                   Gaps
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R; Greco, T.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A; Description: The sequence of C. elegans cosmid K11G9.
A; Reference number: Z20672
A; Accession: T29718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 5
A;Introns: 31/3; 114/3; 144/2; 282/1; 352/1; 460/1
C;Superfamily: cholinesterase; cholinesterase homology
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                                                 5,
                                               Score 43; DB 2
Pred. No. 26;
3; Mismatches
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ilarity 57.1%; Pred. No. 26;
Conservative 3; Mismatches
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Pred. No.
C; Superfamily: hypothetical protein HI0107
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C;Superfamily: hypothetical protein HI0107
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30.8%;
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ilarity 57.1%;
Conservative
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Best Local Similarity 30.89
Matches 12; Conservative
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386 VDTIGGWFLTQNYE 399
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386 VDTIGGWFLTQNYE 399
                                                                                                                                           62 VDSVXGVFLTQNXD 75
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                                               Query Match
Best Local Similarity
Matches 8; Conserv
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Hes 8; Conserv
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A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Accession: C96748
A; Status: preliminary
A; Molecule type: DNA
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A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06222.1; GSPDB:G
A;Experimental source: strain C-125
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; OK, C.; Schluetter, T.; Simces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Tile: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-434 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAD00310.1; PID:916411702; GSPDB:GN00177
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein BH2503 [imported] - Bacillus halodurans (strain C-125)
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C;Superfamily: conserved hypothetical protein H11714
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38.9%; Pred. No. 17;
tive 5; Mismatches
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Pred. No.
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26.1%;
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Matches 12; Conservative
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hes 7; Conserv
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A, Status: preliminary
A, Molecule type: DNA
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A; Map position: 1
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: F96701
C; Accession: Formation: A.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C. C. A.; Li, J. H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Accession: F96701
A; Accession: 
hypothetical protein F16J13.20 - Arabidopsis thaliana (C;Species: Arabidopsis thaliana (mouse-ear cress) (C;Species: Arabidopsis thaliana (mouse-ear cress) (C;Species: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999 (C;Accession: T06602 (C;Accession: T06002 (C;A
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C56748
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudhes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, X.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 41.7%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-738 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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A, Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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A. Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a A. Reference number: A82870
A. Reference number: A82870
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-1131 < GLA>
A. Crossreferences: GB: AE002154; GB: AF222894; NID: g6899557; PIDN: AAF30970.1; GSPDB: GN
C. Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein UU557 [imported] - Ureaplasma urealyticum
C; Species: Ureaplasma urealyticum
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C; Accession: F82875
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, Rebruary 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein ZK892.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28069
R;Lloyd, C.
R;Lloyd, C.
A;Reference number: 220465
A;Reference number: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1131;
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                                                                                                                                                                                                                                        Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 RXFXXWKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 2
A;Introns: 45/1; 105/2; 199/3; 303/2; 382/3; 503/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 RIFSNWANARILVVFVAFITRRWDTASYVCAAISALIFP
                                                                                                                                                                                                                             17.1%; Score 47; DB 50.0%; Pred. No. 5.5; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.4%; Score 45; DB
50.0%; Pred. No. 33;
ive 2; Mismatches
                                                                    A;Gene: yqhB
C;Superfamily: hypothetical protein H10107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 VDTLGGWFLTQNIDAEPESA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      744 FDKYAGSTYDSALGLFLT 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 FXXWKGSVVDSVXGVFLT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 28.29
                                                                                                                                                                                                                                                                                                                                                                                                                                               62 VDSVXGVFLTQNXDXXSSXA
                                                                                                                                                                                                                                                                                Best Local Similarity 50.0
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: UU557
A; Genetic code: SGC3
                                                                                                                                                                                                                                   Query Match
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                      C; Genetics
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C;Species: Bacillus subtilis
S;Species: Bacillus subtilis
S;Species: Bacillus subtilis
S;Species: Bacillus subtilis
S;Species: Bacillus subtilis
C;Species: Bacillu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T32M21.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T44845.
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De Wes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
Ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
Submitted to the Protein Sequence Database, March 2000
A;Reference number: 224487
A;Accession: T48452
A;Accession: T48452
A;Accession: T48452
A;Accession: Freliminary
A;Accession: Frelim
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                                                                                                                                                                                                                                                                                                                                                                                                             418 KVNLDPETIKEWDVLMVNDSPSRSYDDKETEAKWKKEREIFQTRIDLFINRMHRLOGNRK 477
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                              1 KVXXDXXTXXXWXXL-----XXXXDXXXXXXXXXXERXXFXXFXXFXXXFIXRMXXXQGXRX 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            931 KVDIDDETTRIWNLLMGKGDEKEGDEEKDKKKEKWWEEERRVFRGRADSFIARMHLVQG 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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C; Superfamily: Arabidopsis thaliana hypothetical protein F28A23.180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1017;
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                                                                                                           Score 162; DB 2; I
Pred. No. 3.3e-19;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49.5; DB 2;
Pred. No. 5;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 FKQWKGSVVDSVVGVFLTQNTTDYLSSNAFMSVAAKFP 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 FXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                           Query Match 58.9%;
Best Local Similarity 43.9%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.8%;
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A;Introns: 167/1; 874/1
A;Note: T32M21.160
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RESULT 7 T06602

A;Cross-references: GB:299116; GB:AL009126; NID:92634723; PIDN:CAB14406.1; PID:92634909

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

- protein search, using sw model OM protein

2002, 19:24:14 8 November ou:

; Search time 5.88235 Seconds (without alignments) 1470.857 Million cell updates/sec

US-09-840-743-71

Perfect score:

275 1 KVXXDXXTXXXWXXLXXXXD.....TQNXDXXSSXAXMXXAXXFP 90 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 DB DB Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	Н		Ω	hypothetical prote		_		യ	hypothetical prote	_	_	-	S	HlyD family secret	probable periplasm	aminopeptidase N V	probable phosphopr	hypothetical prote	protein	protein	protein	acyltransferase, p	endonuclease III-r	conserved hypothet	hypothetical prote		ε	hypothetical prote
SUMMARIES	QI	D84781	T05430	T48452	E69958	T28069	F82875	T06602	F96701	C96748	683962	AH1353	AI1723	T29718	H72278	AE2799	G97578	G82193	T01385	T30094	WRBP69	WRBP13	JN0031	D81052	G69199	H69874	D84968	T35933	F69826	T24676
	DB	~	7	7	~	7	7	7	N	~	7	7	7	7	7	7	~	7	7	7	Н	Н	7	7	7	~	7	7	7	~
	Length	1207	917	1017	442	541	1131	327	738	217	294	434	434	265	832	432	437	898	894	723	108	108	108	252	253	260	280	319	444	3
	Query	9.5	6.8	8.0	-	7.1				•	5.6	5.6	5.6	5.6	5.6	5.3	5.3	5.3	5.3	5.1	•	4.9	4.9	4.9	6.4	4.9	4.9	4.9	4.9	4.9
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	Score	163.5	162	49.5	47	47	45	Э.	•	43	43	43	43	43	43	42	42	42	42	41.5	41	41	41	41	41	41	41	41	41	41
	Result. No.	Т	7.	cη.	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

myosin IC - slime	RNA polymerase bet	probable lectin pr	qellan lyase (EC 4	preprotein translo	conserved hypothet	hypothetical prote	spou rRNA methylas	probable sugar ABC	citrate (si)-synth	citrate synthase,	glucan 1,4-alpha-q	hypothetical prote	probable heterochr	WD-40 repeat prote	hypothetical prote
T30578	S73652	T40912	T00047	E95237	F98101	B72776	G87396	AG0404	S41563	T49379	T49633	T23238	T37916	AC2239	T00637
~	~	7	7	7	7	7	~	7	7	7	7	7	7	7	7
1181	1391	312	2475	66	66	128	263	329	469	469	748	967	096	1526	1922
14.9	14.9	14.7	14.7	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5
41	41	40.5	40.5	40	40	40	40	40	40	40	40	40	40	40	40
30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	4.5

## ALIGNMENTS

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hypothetical protein At2936490 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Day 18. Day 18. Species: Day 18. Day
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A; Accession: D84781 A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-1207 <STO>
A; Residues: 1-1207 <STO>
A; Cross-references: GB:AE002093; NID:g4581149; PIDN:AAD24633.1; GSPDB:GN00139
C; Genetics:
A; Gene: At2g36490
A; Map position: 2

Gaps 6 DB 2; Length 1207; Indels Score 163.5; DB 2; Pred. No. 2.5e-19; 0; Mismatches 47; 0; 59.58; Conservative Query Match Best Local Similarity Matches 43; Conserv 43;

; ;

500 KVDLDDETDRVWKLLLENINSEGVDGSDEQKAKWWEEERNVFRGRADSFIARMHLVQGDR 559 1 KVXXDXXTXXXWXXL-----XXXXDXXXXXXXXXXXEXXFXXFXXFIXRMXXXQGXR 52 qq δy

90 53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP δy

560 RFTPWKGSVVDSVVGVFLTQNVSDHLSSSAFMSLASQFP qq

RESULT 2

B.; Granderath, K.; Dauner, D.; Herzl, A. October 1998

hypothetical protein F28A23.180 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Accession: 103430 # sequence\_revision 23-Apr-1999 # text\_change 24-Nov-1999 C; Accession: T05430 R; Bevan, M.; Welchselgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; submitted to the Protein Sequence Database, October 1998 A; Reference number: 215415 A; Reference number: 215415

A; Molecule type: DNA A; Residues: 1-917 <BEV> A; Cross-references: EMBL:AL021961

A; Experimental source: cultivar Columbia; BAC clone F28A23

C; Genetics

A;Map position: 4 A;Introns: 41/3; 70/3; 88/1; 118/1; 321/1; 367/1; 474/1; 504/2; 624/3; 655/2; 667/3; A;Note: F28A23.180

us-09-840-743-72.rag

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Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides
                                                                                                                                                                                                               Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.4%; Score 72; DB 23; Length 219; 25.2%; Pred. No. 0.0017; ive 8; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; SEQ ID No 720; 192pp; French.
                                                                                                                                                                         Listeria monocytogenes protein #719.
                                          ABB48015 standard; Protein; 219 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-2001; 2001WO-FR01118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2000; 2000FR-0004629.
                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-010914/01.
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                                                                                                                                                                                                                                                                                                                        WO200177335-A2.
                                                                                                                               05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                  18-OCT-2001
                                                                                    ABB48015;
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RESULT 15
ABB48015
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3;

18;

Local Similarity 25.29

Matches 96

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117 GVGRKTANVVLSVGFGVPAIAVDTHVERISKRLGICRWKDSVVEVEETLKRKLP----- 170 GXGLKSXECVRLLXLXXXAFPVDTNVGRLXVRXGXVPLXPLPXXXQXHXLXXYPXXXXQ 155

156 KXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198

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Search completed: November 8, 2002, 19:25:57 Job time : 38.7026 secs
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Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143,
useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in an Arabidopsis leaf results in expression of the protein in a plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylatycosine glycosylases and regulates
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry -
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                                                                                                                                                                                                                                                                                                     DB 23; Length 166;
5.4e-08;
thes 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lecompte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hyperthermophilic archaeon; hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thierry JC, Prieur D, Dietrich J, I
Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                       Score 98; DB;
Pred. No. 5.4e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           178 ITFGKXXFCTKXXPNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                                                                                                                                                                31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative P. abyssi endonuclease III #1.
                                                                                                                                                                                                                                     sequence represents a DMT-like protein
                                                                                                                                                                                                                                                                                                                                                                                               2 ITFGK-VFCTKRQPNCNACPM-RSECKHFASA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB96207 standard; Protein; 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CNRS ) CNRS CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                       14.1%;
65.6%;
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                                                                                                                                                                                                                                                                                                                        Local Similarity 65.6 tes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-126236/14
                                                                                                                                                                                                                                                                      166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus abyssi.
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Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-2001
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Best Local S
Matches 21
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                                                                                                                                                                                                                                                                        Sequence
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223 AA;

Sequence

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                                                             LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                           LIKLPGIGRKCANIVLAYGFGIPAIPVDTHVYRISRRLGLAPWDASPEEVEERL---- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KXXLLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXX 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 YPXXXXXQKX----LWPRLCKLX-QXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                    Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 218;
                                                                                                                                             ----KELIPR-----EEMIY-VNHAMVDHGK-SVCRPIKPRCDECPL 208
                               50; Indels
                                                                                                                          151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49; Indels
 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ehrlich SD;
DB 22;
7.6e-06;
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Pred. No. 0.00077;
9; Mismatches 49
; Score 86; DB
; Pred. No. 7.66
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; SEQ ID No 1089; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INRG ) INRA INST NAT RECH AGRONOMIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorokine A, Renault P,
                                                                                                                                                                                                                                        ABB54387 standard; Protein; 218 AA
                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis protein nth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.7%;
Best Local Similarity 25.9%;
Matches 30; Conservative
12.4%;
26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-2000; 2000FR-0004630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lactis and related species
                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    Lactococcus lactis IL1403
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-043418/06
           1 Similarity
29; Conserv
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                                                                                                                                                                                                                                                                                                     16-MAY-2002
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                                                                                                                                                                                                                                                                      ABB54387;
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Query Match
Best Local
                                                             91
                                                                                           119
                               Matches
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                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                           ABB54387
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Qγ

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N-PSDB; AAS96697
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                                                                                                           Sequence
                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylotytosine glycosylases and regulates transcription of target genes by demethylation. The present sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to an isolated polynucleotide sequence or their
                                                                                                                                                                             Gaps
                                                                                                                                                             37 IXXRGXXXXLXXRIXXXXXXXXXXXXXXFLXXXVXXXXXXXIDLEWLRXXXXXXXXXXXXXXXX
                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
                                                                                                          Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tatarinova TV;
                                                                                                        Score 141; DB 23;
Pred. No. 2.8e-15;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 86; 109pp; English.
                                                                                                                                                                                                                                                                                                           AAU72747 standard; Protein; 276 AA.
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                                                                                                                                                                                                                            124 LGLKSVECVRLLTLHHLAFPVD 145
                                                                                                                                                                                                               97 XGLKSXECVRLLXLXXXAFPVD 118
                                                                                                          20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0553690.
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                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                      Local Similarity 45.1 les 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                       Corn DMT3 protein.
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                                                                                                                                                                                                                                                                                                                                                              26-FEB-2002
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                                                                                                                                                                                                                                                                                                                                     AAU72747;
                                                                                 Sequence
                                                                                                           Query Match
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                                                                                                                                   Matches
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chromosomal DNA in the cell, reduction of expression of the protein in plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylovytosine glycosylases and regulates transcription of target genes by demethylation. The present sequence represents a DMT-like protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 GXIDLEWLRXXXXXXXXXXXLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 PLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKX-XFCT--- 187
                                                                                                                                                                                                                                                                                                                                                                                                        24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 GKICLEYLRELSVDEVKKELSRFKGIGPKTVACVLMFYLQKDDFPVDTHVLRITKAMGWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                      Length 276;
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                                                                                                                                                                                                                                                                                                                                      , DB 23;
4.2e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                                                                                                                                                                                                                      Score 106;
                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU72746 standard; Protein; 166 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 PATASREKAYIHLNN-------
                                                                                                                                                                                                                                                                                                                                      15.3%;
27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 GSDKRKSSNSACPLAGYCC 268
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DNA demethylation;
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                        276 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in adelay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in a plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylcytosine glycosylases and regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
                                                                                                                                                          882 LGLKSVECVRLLSLHQIAFPVDTNVGRIAVRLGWVPLQPLPDELQMHLL------ 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polynucleotide sequence or their
                                                                 97 XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQK 156
    Gaps
                                      IXXRGXXXXLXXRIXXXXXXXXXXXXXXXXVXXXGXIDLEWLRXXXXXXXXXXXXX 96
  35;
                                                                                                                                                                                                   157 XLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                            Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tatarinova TV;
56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okamuro JK,
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soybean DMT protein related sequence.
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                                                                                                                                                                                                                                                                                                                                             AAU72761 standard; Protein; 179 AA.
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Conservative
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82;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide encoding a DW-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by saxual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in a plant results in enhanced endosperm development and expressing of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising a sequence or C
                                                                                                                                                                  129 GXVPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTK 188
                                                                                                                                 Gaps
                                                                                                                                                                                       2 GWVPLQPLPESLQLHLLELYPVLESIQKYLWPRLCKLDQETLYELHYQMITFGK-VFCTK 60
                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tatarinova TV;
                                                                                         Length 179;
transcription of target genes by demethylation. The present sequence represents a DMT-like protein.
                                                                                         Score 255; DB 23; Length I Pred. No. 2.5e-34; 0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide that control plant development com
having a specific homology to DEMETER domains A,B or
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                                                                                                                                                                                                                                                                                                                                                                             AAU72749 standard; Protein; 145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hannon M,
                                                                                                                                                                                                                                              189 XXPNCNACPMXXXECXXXXSA 209
                                                                                                                                                                                                                                                                               61 SKPNCNACPM-RAECRHFASA 80
                                                                                           36.8%;
63.0%;
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                                                                    Query Match
Best Local Similarity 65.2
Best Local 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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N-PSDB; AAS96699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wheat DMT2 protein.
                                                        179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200180626-A1.
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                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
                                                                                                              156
                                                                                                                           invention relates to an isolated polynucleotide sequence or their
                               Gaps
                                                     37 IXXRGXXXXLXXXXXXXXXXXXXXXXXXXXXX 95
                                                                                                             XGLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQK
                             12;
                                                                                                                                                                                 Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
 Length 1332;
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                                                                                                                                                                 157 XLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXECXXXXSA
                             Indels
                               62;
 DB 23;
 Score 432; DB 23;
Pred. No. 4.1e-63;
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                            0; Mismatches
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                                                                                                                                                                                                                                                             AAU72753 standard; Protein; 251 AA
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62.3%;
55.5%;
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                               Conservative
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                                                                                                                                                                                                                                                                                                                                              protein.
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N-PSDB; AAS96703.
                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max
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                            96;
 Query Match
                 Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
     sample.
                                                                                                                                                                                                                                                                                                                                                                  109 IKERGMNNMLAERI-----OSFLNLLVDKHGGIDLEWLRDVPPDQAKEFLLSIRG 158
                                                                                                                                                                                                                                                                                                                                                                                                                            XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 LGLKSVECVRLLTLHHLAFPVDTNVGRIAVRLGWVPLOPLPESLOLHLLELYPVLESIOK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying plant target proteins for herbicidally active compounds,
                                                                                                                                                                                                                                                                                                              IXXRGXXXXLXXXIXXXXXXXXXXXXFLXXXVXXXGXIDLEWLRXXXXXXXXXXXLLXXXG
The polynucleotide is useful for detecting a nucleic acid in a san Babarrer is related to 5-methylcytosine glycosylases and regulates transcription of target genes by demethylation. The present sequence represents a DMT-like protein.
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                                                                                                                                                                                                 Length 251;
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                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                 DB 23;
                                                                                                                                                                                                                                                     57;
                                                                                                                                                                                              Score 373.5; DB 2
Pred. No. 4.6e-54;
); Mismatches 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herbicidally active_polypeptide SEQ ID NO 1471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 YLWPRLCKLDQRTLYELHYQLITFGK-VFCTK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 XLWPRLCKLXQXTLYELHYXXITFGKXXFCTK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB92260 standard; Protein; 1309
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                                                                                                                                                                                              53.9%;
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                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-269010/31.
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                                                                                                                                          251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FARB ) BAYER AG.
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                                                                                                                                                                                                                                                     . 84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organisms
                                                                                                                                          Sequence
                                                                                                                                                                                                 Query Match
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97 XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQK 156

1554 YLWPRLCKLDQRTLYELHYQMITFGK-VFCTKSKPNCNACPM-RAECKHFASA 1604 g

The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a prometer at least 70% identical to DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a polynucleotide encoding a DMT-like protein. The expression cassette is polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the protein host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following bloodycal activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of the protein in a plant results in an modulation of methylation of chronosomal DNA in the cell, reduction of expression of the protein in an Arabidopsis leaf results in expression of the MEDER general protein in a plant results in expression of the MEDER general to be protein in an Arabidopsis leaf results in expression of the MEDER general teanser general results in expression of the MEDER general to 5-methylcytosine glycosylases and requlates transcription of target genes by demethylation. The present New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA. Tatarinova TV; Length 298; Score 432; DB 23; Pred. No. 8.4e-64; Okamuro JK, Disclosure; Page 88; 109pp; English. AAU72752 standard; Protein; 298 AA. Hannon M, 62.3%; 56.6%; 23-APR-2001; 2001WO-US13059 21-APR-2000; 2000US-0553690 (first entry) (REGC ) UNIV CALIFORNIA Soybean DMT1 protein. Fischer RL, Choi Y, WPI; 2002-055307/07. 298 AA; N-PSDB; AAS96702 WO200180626-A1 26-FEB-2002 Glycine max. 01-NOV-2001 AAU72752; Sequence Query Match RESULT 

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The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide concoding a DMT-like protein and a transgenic plant comprising a polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tatarinova TV;
                                             157 XLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXECXXXXSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 71; 109pp; English.
                                                                                                                                                               AAU72739 standard; Protein; 1332 AA.
                                                                                                                                                                                                                                                               Arabidopsis DMT3 (1DMT3) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-2001; 2001WO-US13059.
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                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi Y,
                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis Thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-055307/07.
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protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in a plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynuclectude is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylcytosine glycosylases and regulates transcription of target genes by demethylation. The present

sequence represents a DMT-like protein.

3;

Gaps

12;

63; Indels

0; Mismatches

98; Conservative

Matches

ô 3

Best Local Similarity

21 IKERGMNNRLADRI------KNFLNRLVEEHGSIDLEWLRDVPPDKAKEYLLSIRG 70

1332 AA;

Sednence

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complement encoding a polypeptide having a sequence at least 40%

Identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B

Co or their combinations. Also included are an expression

corsette comprising the polynucleotide or comprising a heterologous

CD OFF 3. Tlanking sequence, DWT 3. flanking sequence or an 5. untranslated

region of DWT, a host cell comprision an exogenous polynucleotide

concoding a DWT-like protein and a transgenic plant comprising a

concoding a DWT-like protein. The expression cassette is

concoding a DWT-like protein. The expression cassette is

concoding a DWT-like protein. The expression cassette is

cuseful for modulating transcription. The method comprises introducing

the cassette into a host cell with modulated transcription, where

cross, and selecting a host cell with modulated transcription of the

cross, and selecting a host cell with modulated transcription of the

cross, and selecting a host cell with modulated transcription of

cross, and selecting a cell results in a modulation of the following

blological activities, which include enhanced expression of the

protein in a plant results in modulation of expression of the protein in a

plant results in enhanced endosperm development and expressing of the

cross protein in an Arabidopsis leaf results in expression of the MEDEA gene.

The polynucleotide is useful for detecting a nucleic acid in a sample.

CT The polynucleotide is useful for detecting a nucleic acid in a sample.

CT The DEMETER is related to 5-methylcycosine glycosylases and expensent

cross or sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                            New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polynucleotide sequence or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 WLRXXXXXXXXXXXXXCXLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXGXVPLXPLP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 XXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.5%; Score 433; DB 23; Length 1729;
51.0%; Pred. No. 3.7e-63;
ive 0; Mismatches 82; Indels 12
                                                                                                                                                                                                                                                   Tatarinova TV;
                                                                                                                                                                                                                                                   Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 54-55; 109pp; English.
                                                                                                                                                                                                                                                Choi Y, Hannon M,
                                                                                                           23-APR-2001; 2001WO-US13059.
                                                                                                                                                       21-APR-2000; 2000US-0553690.
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                                                                                                                                                                                                                                                                                             WPI; 2002-055307/07
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                  WO200180626-A1.
                                                                                                                                                                                                                                                   Fischer RL,
                                                                 01-NOV-2001
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The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATRODOS (ATR)) Domain A, B crossette comprising the polynucleotide are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a prometer at least 70% identical to DMT 5′ flanking sequence, DMT 3′ flanking sequence or an 5′ untranslated region of DMT, a host cell comprising an exogenous polynucleotide concoding a DMT-like protein and a transgenic comprising a polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassettee into a host cell preferably Agrobacterium by sexual the protein is capable of exhibiting at least one of the following the protein in a plant results in adelay in flowering time, introduction of the protein in a plant results in adelay in flowering time, introduction of the protein in an Arabidopsis leaf results in expression of the protein in an Arabidopsis leaf results in expression of the MEDER general The polynucleotide is useful for detecting a nucleic acid in a sample. The polynucleotide is useful for detecting a nucleic acid in a sample. The polynucleotide is useful for detecting a nucleic acid in a sample. Sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 12;
                                                                                                             Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1952;
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Pred. No. 4.2e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                     Okamuro JK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.5%;
55.5%;
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                                     26-FEB-2002 (first entry)
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                                                                          Rice DMT1 protein.
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                                                                                                                                                                                          Oryza sativa
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AAU72743 standard; Protein; 1952 AA.

AAU72743

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Arabidopsis Thaliana.
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                                   The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at lesst 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or C or their compliations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a prometer at least 70% identical to DMTs flanking sequence, DMTs flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exceptions polynucleotide encoding a DMT-like protein and a transgenic plant comprising a coording a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein in a plant results in a delay in flowering the protein in a plant results in adelay in flowering the protein in a plant results in modulation of methylation of the protein in an Arabidopsis leaf results in expression of the protein in a hanneed endosperm development and expressing of the C protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. Secondary corresponds and requiates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        874 EKTRSTMDTVDWKAIRAADVKEVAETIKSRGMNHKLAERIQYLTLNMKIMOGFLDRLVND 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 XGXIDLEWLRXXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXXXXAFPVDTNVGRIXVRXGX 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 VPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXX 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                          Score 440; DB 23; Length 1413;
Pred. No. 2e-64;
0; Mismatches 98; Indels 2
                                                                                                                                                                                                                                                                                                                                                       sequence represents a DMT-like protein
               Disclosure; Page 67; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU72741 standard; Protein; 1114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis DMT4 (1DMT4) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                          / Match 63.5%;
Local Similarity 49.7%;
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                                                                                                                                                                                                                                                                                                                                                                               1413 AA;
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complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMTER, previously known as ATROPOS (ATR)) Domain A, B corrected to complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMTER, previously known as ATROPOS (ATR)) Domain A, B cr C or their comprising the polymucleotide or comprising a heterologues polynucleotide under the control of a promoter at least 70% identical to DMT 5. flanking sequence, DMT 3. flanking sequence or an 5. untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein. The expression cassette is polymucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. The polynucleotide is useful for detecting a nucleic acid in a sample. The polynucleotide is a DMT-like protein. The present
                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated polynucleotide sequence or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQK 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 705 YLWPRLCKLPQETLYELHYQMITFGK-VFCTKTIPNCNACPM-KSECKYFASA 755
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62.5%; Score 433; DB 23; Length 1114;
Best Local Similarity 55.5%; Pred. No. 2.3e-63;
Matches 96; Conservative 0; Mismatches 65; Indels 12;
                                                                                                                                                                   Tatarinova TV;
                                                                                                                                                                   Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 75; 109pp; English.
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21-APR-2000; 2000US-0553690
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                                                                                    (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                   Choi Y,
                                                                                                                                                                                                                                               WPI; 2002-055307/07.
N-PSDB; AAS96694.
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8, 2002, 19:24:08; Search time 35.7026 Seconds (without alignments) 858.415 Million cell updates/sec
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*/SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:
*/SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:
*/SIDSZ/gcgdata/geneseqg-emb2/AA1985.DAT:
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*/SIDSZ/gcgdata/geneseqg-emb1/AA1986.DAT:
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
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693
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STIMMARTES

SOMMAKIES		Description							AAU72753 Soybean DMT2 prote			
		B ID	23 #	23 2	23 F	23 7	23 2	23 #	23 P	23 #	23 #	23 F
		Query Match Length DB	1413	1114	1729	1952	298	1332	251	1309	179	145
	æ	Query	63.5	62.5	62.5	62.5	62.3	62.3	53.9	48.4	36.8	20.3
		Score	440	433	433	433	432	432	373.5	335.5	255	141
		Result No.	 П	7	Э	4	5	9	7	80	6	10

New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or  ${\tt C}$ 

-	901	15.3	276	23	AAU72747	Corn DMT3 protein.
12	86	14.1	166	23	AAU72746	
13	98	2	223	22	S	o, abyss
14	74	٠.	218	23	~*	cus lact
15	72	0	219	23	ABB48015	nocyto
16	89		210	22	AAG81939	<ol> <li>S. epidermidis ope</li> </ol>
17	89		224	22	AAG82795	. epidermidis
18	29		224	23	ABP38380	scas
19	63		308	22	ABB58227	mela
20	61		1072	22	ABB69797	
21	59		350	19	AAW60244	U
22	59		350	22	AAU69755	Escherichia coli (
3 5			118	21	AAB37443	Human cystatin D.
4 5	•		122	21	AAY81137	Human wild-type cy
5			122	21	AAY81171	mutant cys
9	•		122	21	AAY81172	
7 5			122	21	AAY81173	Human mutant cysta
8			122	21	AAY81174	
9	•		122	21	AAY81175	Human mutant cysta
0 5			122	21	AAY81176	
1 5	7.5		122	21	AAY81177	
2	•	•	122	21	AAY81181	c
3 5			122	21	AAY81182	mutant
4 5		•	142	22	AAE11210	cystatin D
5			142	22	AAE04437	cystati
9			142	22	AAE02408	Human cystatin D p
7 5			142	23	AA015149	Human cystatin D p
8			122	21	AAY81178	ų
39	26		195	21	AAG12675	1
40	26		326	21	AAG12674	Arabidopsis thalia
1 5			320	19	AAW70220	Leishmania antigen
2	•		320	19	AAW70236	Leishmania antigen
3 5	5.5		320	23	ABG60872	Leishmania antigen
5			320	23	ABG60888	Leishmania antigen
5			320	23	AAU71816	Leishmania antigen
					ALTGNMENTS	
AAU72737						
FD AAU72737		standard:	Protein: 1413	in:	1413 AA.	

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Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
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                                                                                                  AAU72737 standard; Protein; 1413 AA.
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George W.

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                    --- 74
                                                                                                                                                                                             Sequence 36, Application US/08808550
Patent No. 5871992
GENERAL INFORMATION:
APPLICANT: Teebor, George W.
APPLICANT: Hilbert, Timothy P.
TITLE OF INVENTION: MAMMALIAN ENDONUCLEASE III AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 207;
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                                                        155 OKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXEC 203
                                                                                   ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,550
FILING DATE: 26-FEB-1997
CLASSIFICATION: 435
38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.0%; Score 48.5; DE 23.4%; Pred. No. 5.9; Ative 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 ------QPINHLLVGFGQMQ-CQPVRPKCGTC 197
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ATTONNEY FAGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-808-550-39; Sequence 39, Application US/08808550; Patent No. 5871992
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Best Local Similarity 23.4%
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07601
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                                                                                                                                                                          US-08-808-550-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 ECVRLLXLXXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQKXLWPRL 162
APPLICANT: Hilbert, Timothy P.

TITLE OF INVENTION: MAMMALIAN ENDONUCLEASE III AND

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: Bavid A. Jackson, Esq.
STREET: Floor

CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 48.5; DB 2; Length 259; llarity 23.4%; Pred. No. 7.4; Conservative 7; Mismatches 38; Indels 2'
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,550

FILING DATE: 26-FEB-1997
CLASSIFICATION: 435
ATTONNEY/AGBNT INFORMATION:
NAME: Jackson Esq., 26,742
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-001 N
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 39:
SEQUENCE CRARACTERISTICS:
LENGTH: 259 anino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8, 2002, 19:29:16
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO FRAGMENT TYPE: N-termin ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: November
Job time: 15.1536 secs
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Matches 22; Conserva
                                                                                                                                                                                                                                                 STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-808-550-39
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Gaps

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96 GXGLKSXE-CVRLLXLXXXAFFVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Steven G.
APPLICANT: Campos Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                            Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55.5; DB 4; Length 320;
Pred. No. 0.7;
7; Mismatches 30; Indels 5
                                                                                                                                                                                                                                                                                                                                                                          155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXEC 203
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUBER: US/No.^^
                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                            Score 55.5; DB 4;
Pred. No. 0.7;
                                                                                                                                                                                                                                                                                                                     34 GYGLTSSSVCVRCSVAGCKSCPVDANVCKVCL-GGSEPINNM-
                                                                                                                                                                                                                                                    7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 55, Application US/09022765; Patent No. 6375955; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                            Query Match 8.0%;
Best Local Similarity 19.3%;
    (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%;
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                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                               LENGTH: 320 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 320 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                    Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.0°
Best Local Similarity 19.3°
Matches 21; Conservative
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                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-765-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Campos Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND NUMBER OF SEQUENCES: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.0%; Score 55.5; DB 4; Length 320; 19.3%; Pred. No. 0.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXEC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/09/183,861
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSEE: SEED and BERRY LLP
F: 6300 Columbia Center, 701 Fifth Avenue
Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DAME: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELEFONMUNICATION INFORMATION:
TELEFONDE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE GIRRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/09022765
Patent No. 6375955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 12-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 320 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 19.37
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITA.
STATE: Was...
COUNTRY: USA
TO 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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CITY: Se
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96 GXGLKSXE-CVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 154
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Patent No. 6365165
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND NUMBER OF SEQUENCES: 87
CORRESPONDENCE SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and TITLE
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55.5; DB 4; Length 320;
Pred. No. 0.7;
7; Mismatches 30; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXEC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                             E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.0%;
Best Local Similarity 19.3%;
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 320 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-183-861-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-7092
COMPUTER READABLE FORM
                                                                                                                                                                                                                          Washington
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                                                                                                                                                                                                                                                                98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seattle
                                                                                                                                                                                                       Seattle
                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
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                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 8.3%; Score 57.5; DB 4; Length 142; Best Local Similarity 41.7%; Pred. No. 0.14; Matches 10; Conservative 4; Mismatches 9; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                   APPLICANT: Gentz, Reiner L.
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: Human Cystatin E
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DCKET NUMBER: PF202P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301 309 8504
TELEFAX: 301 309 8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/241,376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/744,138
FILING DATE: 05-NOV-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
PPPLICATION NUMBER:
PPLLICATION NUMBER:
05-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; INDIVIDUAL ISOLATE: Cystatin D US-09-241-376-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 HYXXITFGKXXFCTKXXPNCNACP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/09183861
Patent No. 6365165
GENERAL INFORMATION:
                                          84 YYFNVKFGRTT-CTKSQPNLDNCP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Reed, Steven G. APPLICANT: Campos-Neto, Antonio
                                                                                                                                         Sequence 4, Application US/09241376
Patent No. 6300477
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 142 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 301 309 8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-183-861-22
                                                                                                                      US-09-241-376-4
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8.3%; Score 57.5; DB 3; Length 142; 41.7%; Pred. No. 0.14;
                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                              84 YYFNVKFGRTT-CTKSQPNLDNCP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 HYXXITFGKXXFCTKXXPNCNACP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 HYXXITFGKXXFCTKXXPNCNACP 197
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                                                                                                                                                                                                                                     Sequence 7, Application US/09431480 Patent No. 6235708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application \text{US/09617302} Patent No. 6245529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.3%;
Best Local Similarity 41.7%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 41.79
Matches 10; Conservative
                                        Best Local Similarity 41.79
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-617-302-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-617-302-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-431-480-7
                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                      3;
TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA TITLE OF INVENTION: MISMATCHES
                                                                                                                                                                                                                                                                                                                                                                          96 GXGLKSXECVRLLXLXXXAFPV-DTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXX 154
                                                                                                                                                                                                                                                                                                                                                                                                                 -----CYAVSGWPGKKEV 160
                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                DB 4; Length 350;
                                                                                                                                                                                                                                                                                                                                      53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDICUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NATA:
APPLICATION NUMBER: US/08/744,138
                                                                                                                                                                                                                                                                                              Score 59; DB 4
Pred. No. 0.21;
                          TILLE CETTERNOET IL-10284
CURRENT APPLICATION NUMBER: US/09/650,855
CURRENT FILING DATE: 2000-08-29
PRIOR PILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 37
LENGTH: 350
                                                                                                                                                                                                                                                                                                                                    14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6

US-08-744-138-4

Sequence 4, Application US/08744138

Settent No. 6011012

GENERAL INFORMATION:
APPLICANT: Gentz, Reiner L.
APPLICANT: Ni, Jian
SPELICANT: No. Jian
TITLE OF INVENTION: Human Cystatin E
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human C--
STREET.
                                                                                                                                                                                                                                                                                                                                                                                                               116 GVGRSTAGAILSLSLGKH-FPILDGNVKRVLAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE: Cystatin D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: BROACES, A. AnderS
REGISTRATION NUMBER: 30,373
REFERENCE/DOCKET NUMBER: PF2/
TELECOMUNICATION INFORMATION:
TELEPHONE: 301 309 8504
TELEFRAX: 301 309 8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36,373
                                                                                                                                                                                                                                                                                              Query Match 8.5%;
Best Local Similarity 20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                    21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 142 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: Escherichia coli
US-09-650-855-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 9410 Key CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-08-744-138-4
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Gaps
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CURRENT APPLICATION NUMBER: US/09/617,302
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 60/109,217
PRIOR APPLICATION NUMBER: 60/109,217
PRIOR PILING DATE: 1998-11-01
PRIOR PILING DATE: 1998-11-01
PRIOR APPLICATION NUMBER: 60/156,382
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                    GENERAL INCORNATION:
APPLICANT: Holloway, James L.
APPLICANT: Holloway, James L.
APPLICANT: Fedidaus, Andrew
TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
FILE REFERENCE: 98-72
CURRENT APPLICATION NUMBER: US/09/431,480
CURRENT FILING DATE: 1999-11-01
EARLIER APPLICATION NUMBER: 60/109,217
EARLIER APPLICATION NUMBER: 60/156,382
EARLIER FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
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11.7%; Pred. No. 0.14;
ive 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.3%; Score 57.5; DB 4; Length 142; 41.7%; Pred. No. 0.14;
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REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: AT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                  INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 350 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Escherichia coli
US-09-651-656-37
                                                                                                 TELEFAX: 610-270-4026
                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-813-574-9
  Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-09-651-656-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 37
LENGTH: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 LLXXXGXGLKSXECVRLLXLXXXAAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 LVKLPGVGRKTANVVVSVAFGVPAIAVDTHVERVSKRLGICRWKDSVLEVEKTLMRKVP- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.2%; Score 64; DB 2; Length 209; Best Local Similarity 23.1%; Pred. No. 0.02; Matches 25; Conservative 10; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 -----KEDWS------VTHHRLIFFGR-YHCKAQSPRCAECPL 201
                                                                                            COMPOUR: IBM PC compatible
COMPOURS: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FAPILCATION NUMBER: US/08/808,550
FILING DATE: Z6-FEB-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08813574;
Patent No. 6013473;
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
TITLE OF INVENTION: Human Muty
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/813,574
                                                                                                                                                                                                                                                                                                       1049-1-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/013,132
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bacillus subtilis US-08-808-550-31
                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                             209 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19406
COMPUTER READABLE FORM:
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PA
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                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-813-574-9
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APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MCCUTHEN MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERRORE NATIONAL LABORATORY
APPLICANT: LAWRENCE LIVERRORE NATIONAL LABORATORY
TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLECTIDE
TITLE OF INVENTION: DOLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,
TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
FILE REFERENCE: 1L-10609
CURRENT APPLICATION NUMBER: US/09/651,656
CURRENT FILING DATE: 2000-08-29
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATCHIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 GVGRSTAGAILSLSLGKH-FPILDGNVKRVLAR-------CYAVSGWPGKKEV 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.5%; Score 59; DB Best Local Similarity 20.2%; Pred. No. 0.21 Matches 21; Conservative 14; Mismatches
ATG50002
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108-09-650-855-37
Sequence 37, Application US/09650855
Patent No. 6365355
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CITY: Hackensack
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Sequence 52
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                                                                                                                                                                          2002, 19:24:15; Search time 13.1536 Seconds (without alignments) 514.481 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                  Description
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5.1.3
Compugen Ltd
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US-09-651-656-37
US-09-744-138-4
US-09-431-480-7
US-09-617-302-7
US-09-183-861-22
US-09-022-765-25
US-09-022-765-55
US-08-08-550-36
US-08-08-550-36
US-08-08-550-36
US-08-744-138-3
US-08-744-138-3
US-08-744-138-3
US-08-744-138-3
US-08-744-138-3
US-09-019-485-4
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US-09-019-485-4
US-09-019-481-4
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US-08-974-022-52
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         GenCore version
Copyright (c) 1993 - 2002
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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693
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Maximum DB
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No.
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Sequence 3225, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT PILICIG DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PROR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3225
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                                                  Sequence 139, App
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 2, Appli
Sequence 3, Appli
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   Sequence
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Patent No. 5871992
GENERAL INFORMATION:
APPLICANT: Teebor, George W.
TITLE OF INVENTION: MAMMALIAN ENDONUCLEASE III AND
TITLE OF INVENTION: DAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
US-08-795-445A-52
US-08-795-447A-52
US-08-795-446B-52
US-08-795-446B-52
US-08-26-139
US-08-26-139
US-09-150-86A-6
US-09-12-269A-2
PCT-US96-03965-2
US-08-012-269A-2
US-08-013-574-2
US-08-13-574-2
US-08-13-574-2
US-08-13-574-2
US-09-241-376-7
US-09-241-376-7
US-09-241-376-7
US-09-241-376-7
US-09-619-062-2
US-09-619-062-2
US-09-619-062-2
US-09-619-062-2
US-09-619-062-2
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Pred. No. 0.007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 9.7%;
1 Similarity 22.1%;
23; Conservative 1:
 Best Local Similarity
   US-09-134-001C-3225
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US-08-808-550-31
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 Query Match
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Gaps
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Sequence No. US20020137611A1
GENERAL INFORMATION:
APPLICANT: University of British Columbia
TITLE OF INVENTION: Production and use of Modified Cystatins
FILE REFERENCE: 58069
CURRENT APPLICATION NUMBER: US/09/775,932
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 1999-08-05
PRIOR PLICATION NUMBER: GA99/00717
PRIOR FILING DATE: 1999-08-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO. 6
LENGTH: 121
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                    OTHER INFORMATION: MAP TO ACO11301.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HEBLIOO, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HERRY, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN FIGNAL LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN FIGNAL SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN FIGNAL LIVER, SIGNAL = 1.2

OTHER INFORMATION: EST_HUMAN HIT: AA306508.1, EVALUE 2.40e+00

US-09-864-761-35736
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                                                                                                                                                                                                                 6.5%; Score 45; DB 10; Length 84; 50.0%; Pred. No. 2.4; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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Best Local Similarity 2/...
Best Local 10; Conservative
                                                                                                                                                                                                                                                  Conservative
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Job time: 8.14052 secs
       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                              187 TKXXPNCNACPM 198
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; ORGANISM: Homo sapiens
US-09-775-932-6
                                                                                                                                                                                                                                                                                                          33 SQLAPNCTACPL 44
                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
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US-09-775-932-6
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                                                                                                                                          Length 494;
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                                                                                                                                       Query Match 6.6%; Score 45.5; DB 10; Best Local Similarity 32.4%; Pred. No. 14; Matches 11; Conservative 6; Mismatches 16;
                                                                                                                                                                                                   104 CVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLP 137
                                                                                                                                                                                                                      319 CAQMLAMVSLPFYLQTVLGRSEVETGLL-LTPWP 351
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 468
LENCTH: 494
                                                                            TYPE: PRT
ORGANISM: Escherichia coli
US-09-741-669-468
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US-09-864-761-35736
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (438)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REPERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                     Query Match 6.9%; Score 47.5; D
Best Local Similarity 33.3%; Pred. No. 1.7;
Matches 8; Conservative 5; Mismatches
                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,834
FILING DATE: 01-Oct-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-969-834-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-925-301-1326
Sequence 1326, Application US/09925301
; Patent No. US20020052308a1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 HYXXITFGKXXFCTKXXPNCNACP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                    Diskette
                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1326
LENGTH: 486
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APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
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                                                                                                             3;
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-301-1326
                                                                                                                                                       96 GXGLKSXECVRLLXLXXXAFPVDTNVGRLXVRXGXVPLXPLPXXXQXHXLXXYPXXXXXQ 155
                                                                                                                                                                                                 225 GVGRYTAGAIASIAFGQATGVVDGNVARVLCR-------VRAIGADPSSTLVS 270
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                                                                                                             16;
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6
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                                                                   Length 486;
                                                                                                             Indels
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Fatent No. US2002022718A1
GENERAL INFORMATION:
APPLICANT: FORSYCHO:
APPLICANT: Oblsen, Karl L.
APPLICANT: Oblsen, Karl L.
APPLICANT: Oblsen, Karl L.
APPLICANT: Oblsen, Karl L.
TILE OF INVENTION: Genes identified as required for TTLE OF INVENTION: proliferation of E. coll
FILE REFERENCE: ELITRA, 009A
CURRENT FILIGE DATE: 2000-12-19
CURRENT FILIGE DATE: US 60/173005
                                                                                                                                                                                                                                             156 KXLWPRLCKLXQ-XTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                         271 QQLWGLAQQLVDPARPGDFNQAAMELG-ATVCTPQRPLCSQCPV 313
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19;
                                                                   10;
                                                                 6.6%; Score 46; DB 1
18.3%; Pred. No. 12;
tive 12; Mismatches
                                                          DB '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.6%; Score 46; DB
ilarity 46.2%; Pred. No. 19;
Conservative 1; Mismatches
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CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SEQ ID NO 224
LENGTH: 758
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Royer, John
Salama, Sofie
Sherman, Amir
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 224, Application US/09801368 Patent No. US20020128250A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Saccharomyces cerevisiae US-09-801-368-224
                                                                 Query Match 6.6%
Best Local Similarity 18.3%
Matches 19; Conservative
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Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cali, Brian
Hecht, Peter
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Milne, Todd
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Best Local Similarity
Matches 12; Conserva
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APPLICANT: Busby, R
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APPLICANT:
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APPLICANT:
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ORGANISM:
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Gaps
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                                                                                                                                                                                                                                                                                                         Length 120;
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Patent No. US20020102711A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Goli, Surya K.
TITLE OF INVENTION: PROTEIN
PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47.5; DB 10;
Pred. No. 1.7;
5; Mismatches 10;
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ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
CITY: CA
COUWRY: GA
ZIP: 94304
                                                                                                                                                                                                                                                                                                         Score 47.5; DB Pred. No. 1.4; 5; Mismatches
CURRENT APPLICATION NUMBER: US/09/775,932
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: CA99/00717
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 120
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Sequence 3, Application US/09940497

; Patent No. US20020052476A1

; GENERAL INPORMATION:
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ilarity 33.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-09-775-932-2
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Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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US-09-969-834-3
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                      APPLICANT: Ruben et al. ITLE OF INVENTION: Calcium Channel Polynucleotides, Polypeptides, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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APPLICANT: Rosen et al.
TITLE OF INVENTION: NUCleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC055
CURRENT FILING DATE: 2001-01-17
Prior application data removed · refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1188
LENGTH: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.9%; Score 47.5; DB 10; Length 82; 22.2%; Pred. No. 0.91; ive 10; Mismatches 34; Indels
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APPLICANT: University of British Columbia
TITLE OF INVENTION: Production and use of Modified Cystatins
FILE REPERENCE: 58069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Pred. No. 2.6;
2; Mismatches 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 LLPRMASLG-LTLLIFYYSFAIVGMEFFCGIVFPNC 365
                                                   TITLE REPERENCE: PT0139121
CURRENT APPLICATION NUMBER: US/10/050,786
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 09/774,028
PRIOR APPLICATION NUMBER: US 09/774,028
PRIOR PILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: PCT/US00/20392
PRIOR PILING DATE: 2000-07-27
PRIOR PILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-08-18
PRIOR FILING DATE: 1999-08-18
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
SOFTWARE: PATENTIN NOWBER: US 60/189,064
PRIOR FILING DATE: 2000-03-14
SOFTWARE: PATENTIN OFF: 13.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.3%;
Best Local Similarity 36.1%;
Matches 13; Conservative ;
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Best Local Similarity 22.2°
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Homo sapiens
US-10-050-786-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-877-1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-764-877-1188
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APPLICANT: Probst, Peter
APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: LEISHMANIA AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.42008
CURRENT APPLICATION UNMBER: US/09/874,923
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 320
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US-09-874-923-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 121, Application US/09874923; Patent No. US20020081320A1; GENERAL INFORMATION: APPLICANT: Reed, Steven G.
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; Patent No. US20020155539A1
                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Leishmania major US-09-874-923-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 21; Conserva
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US-09-874-923-121
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US-10-050-786-7
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                                                                                                                                                                                                                                                                                                                                                              Gaps
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Sequence 2.3 Application US/09874923

Patent No. US20020081320A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Campos-Mato, Antonio

APPLICANT: Webb, John R.

APPLICANT: Blatia, Ajay

APPLICANT: Bhatia, Ajay

APPLICANT: Bratia, Ajay

APPLICANT: Bratia, Ajay

APPLICANT: Brannon, Mark

TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE

TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE

TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE

TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE

TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE

TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE

TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE

TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE

TITLE OF INVENTION: LEISHMANIA ANTIGENS OF LEISHMANIASIS

CURRENT FILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 122

SOFTWARE FERSEE FASTSEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                        Length 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 ------CPCTDDNCASCPSDAGTC 92
                                                                                                                                                                                                                                                                                                        Query Match 8.3%; Score 57.5; DB 10; Length Best Local Similarity 41.7%; Pred. No. 0.037; Matches 10; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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PRIOR FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: US 08/744,138
PRIOR FILING DATE: 1996-11-05
PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 55, Application US/09874923
Patent No. US20020081320A1
GENERAL INPOMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                            84 YYFNVKFGRTT-CTKSQPNLDNCP 106
                                                                                                                                                                                                                                                                                                                                                                                                    174 HYXXITFGKXXFCTKXXPNCNACP 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Leishmania major
US-09-874-923-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-940-497-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-874-923-22
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                                                                                                                                                                                         LENGTH: 142
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                                                                                                      96 GXGLKSXE-CVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Campos-Netco, Antonio
APPLICANT: Campos-Netco, Antonio
APPLICANT: Webb, John R.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Bratia, Ajay
APPLICANT: Brannon, Mark
APPLICANT: Probst, Peter
APPLICANT: Probst, Peter
APPLICANT: Tribe of INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: LEISHMANIA ANTIGENS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C8
CURRENT APPLICATION NUMBER: US/09/874,923
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 709
Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 709;
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                                                                                                                                                                                                          155 QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPMXXXEC 203
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                                                                                                                                       423 GYGLTSSSVCVRCSVAGCKSCPVDANVCKVCL-GGSEPINNM----
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ilarity 19.3%; Pred. No. 0.47;
Conservative 7; Mismatches 30;
                                                   30;
     DB 10;
Query Match

8.0%; Score 55.5; Di
Best Local Similarity 19.3%; Pred. No. 0.2;
Matches 21; Conservative 7; Mismatches
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Sequence 5, Appli Sequence 1, Appli Sequence 776, App Sequence 37, App Sequence 607, App Sequence 607, App Sequence 652, App Sequence 464, App Sequence 46, Appli Sequence 34, Appli Sequence 349, Appli Sequence 340, Appli Sequence 340, Appli Sequence 2, Appli

equence 141, App Sequence 5, Appli

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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Sequence 10, Application US/09775932

Patent No. US20020137671A1

GENERAL INFORMATION:

APPLICANT: University of British Columbia

TITLE OF INVENTION:

TITLE OF INVENTION: Production and use of Modified Cystatins

FILE REFERENCE: 58069

CURRENT APPLICATION NUMBER: US/09/775,932

CURRENT FILING DATE: 1099-08-05

PRIOR FILING DATE: 1999-08-05

PRIOR APPLICATION NUMBER: 60/095,503

PRIOR FILING DATE: 1999-08-05

NUMBER OF SEQ ID NOS: 32

SOFTWARRE: Patentin Ver: 2.0

SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 122;
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US-09-943-388-5

US-09-818-954A-1

US-09-147-155-387

US-09-748-85-17

US-09-76-85-17

US-09-76-85-17

US-09-76-85-17

US-09-76-889-283

US-09-76-889-283

US-09-76-899-283

US-09-76-899-283

US-09-76-899-283

US-09-76-864-761

US-09-77-15-360

US-09-77-15-360

US-09-77-15-360

US-09-76-8826-40

US-09-76-8826-40

US-09-76-8826-40

US-09-76-8826-40

US-09-76-8826-89
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US-09-909-280A-2
US-09-808-602-67
US-09-775-932-24
US-09-775-932-4
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8.3%; Score 57.5; DB 1
Best Local Similarity 41.7%; Pred. No. 0.031;
Matches 10; Conservative 4; Mismatches
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US-09-940-497-5
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APPLICANT: Ni et al.
TITLE OF INVENTION: Human Cystatin E
FILE REFERENCE: PF202P1D2
CURRENT APPLICATION NUMBER: US/09/940,497; CURRENT FILING DATE: 2001-08-29; PRIOR APPLICATION NUMBER: US 09/241,376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 YYENVKFGRTT-CTKSQPNLDNCP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-09-775-932-10
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Sequence 22, Appli
Sequence 22, Appli
Sequence 121, Appli
Sequence 118, Appli
Sequence 118, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 324, Appli
Sequence 224, Appli
Sequence 325, Appli
Sequence 325, Appli
Sequence 35736, Appli
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Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
                                                                                                                                 2002, 19:26:04; Search time 7.14052 Seconds (without alignments) 464.428 Million cell updates/sec
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                                                                                                                                                                                                                                                       Published_Applications_AA:*

| cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
                      GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-764 877-1188
US-09-75-932-2
US-09-940-497-3
US-09-969-834-3
US-09-925-301-1326
US-09-801-368-224
US-09-741-669-468
US-09-775-932-6
US-09-940-497-7
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0 US-09-940-497-4

0 US-09-874-923-22

0 US-09-874-923-55

0 US-09-874-923-121

US-10-050-786-7
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US-09-943-388-2
                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-943-388-9
                                                                                                                                                                                                                                                                                                                                                    92612 seqs, 14418503 residues
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                                                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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Match Length DB
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1;

Gaps

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Result

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5;
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      SMART; SM00478; ENDO3c; 1.

      SMART; SM00525; EES; 1.

      PROSITE; PS00764; ENDONUCLEASE_III_1; 1.

      PROSITE; PS01155; ENDONUCLEASE_III_2; 1.

      Hypothetical protein; DNA repair; Hydrolase; Glycosidase; Lyase; Iron-sulfur; 4Fe-4S.

      METAL
      187

      METAL
      194

      197
      IRON-SULFUR (4FE-4S) (BY SIMILARITY).

      METAL
      197

      187
      IRON-SULFUR (4FE-4S) (BY SIMILARITY).

      METAL
      203

      180
      SUBLEUR (4FE-4S) (BY SIMILARITY).

      SEQUENCE
      259 AA; 28841 MW; F52E57810571EDBC CRC64;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 CKLXQXTLYELHYXXITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: November 8, 2002, 19:27:11 Job time : 10.268 secs
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"The genome sequence of Schizosaccharomyces pombe.";
                                 Nacure 412:8/1-880(2002).
-i- SUBGELLULAR LOCATION: Nuclear (By similarity).
-i- SIMILARITY: BELONGS TO THE UPF0202 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2;
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P54137;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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RA WOOD V., GWILLIAM R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,
RA Squuros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones L., Jones M., Eather S., McDonald S., McLean J.,
RA Janor P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA A Hutherford K., Rutter S., Saudares R., Slarp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aslares R., Scheefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Scheefer M., Mueller-Auer S.,
Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gable C., Fuchs W., Wedler H., Rambutt R., Pohl T.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., Morcon S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                 "Nucleotide sequence of the essential region of bacteriophage P4.";
Nucleic Acids Res. 12:8667-8684(1984).
-!- SIMILARITY: SOME, TO E.COLI PROPHAGE CP4-57 REGULATORY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 PLXPLPXXXQXHXLXXYPXXXXXQKXLWP---RLCKLXQXTLYEL 173
                                                                                                                                                                                                                                                                                                                                EMBL; X51522; CAA35903.1; -.
EMBL; X02534; CAA26377.1; -.
PIR; G23878; Q1BPP4.
PIR; JW0029; JW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
19-JUL-1001 protein C2068.09c in chromosome 1
SPAC2068.09C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49.5; DB Pred. No. 0.69; 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Les 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDK9_SCHPO
P87115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDK9_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
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-!- FUNCTION: HAS BOTH AN APURINIC AND/OR APYRIMIDINIC ENDONUCLEASE
ACTIVITY AND A DNA N-GIXCOSYLASE ACTIVITY (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or apyrimidinic site in DNA is broken by a beta-elimination reaction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leaving all terminal unsaturated sugar and a product with a terminal 5'-phosphate.
-!- COFACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE CATALYTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER POSITIONING OF THE BRAYME ALONG THE DNA STRAND (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
16-077-2001 (Rel. 40, Last annotation update)
Probable endonuclease III homolog (EC 4.2.99.18) (DNA-(Apurinic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.1%; Score 49; DB 1; Length 1033; 27.9%; Pred. No. 9.1; Live 6; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       282 289 ATP (POTENTIAL).
1033 AA; 116463 MW; 8432B313DB18E135 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 KXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        691 KTMPPLLLKLSELQPEPLHYVGVSYGLTPSLQKFWKREGYCPL 733
                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; ATP-binding; Nuclear protein. NP_BIND 282 289 ATP (POTENTIAL).
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InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR004035; EndoIII_HHH.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003651; FeS_bind.
Pfam; PF00730; HhH-GPD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z50874; CAA90766.1; -. HSSP; P20625; ZABK.
                                                                                                                                                                                                                                                                                                                                       EMBL; 295334; CAB08603.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apyrimidinic site) lyase). R10E4.5.
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Matches 12; Conservative
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9

92 Matches

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                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                             01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 119.3 kDa protein in FPR1-TOM22 intergenic region.
YML132W OR N1216 OR N1858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.4%; Score 51; DB 1; Length 1056; 30.2%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (POTENTIAL).
M; 76721ED0867ED618 CRC64;
                                                                                                                                                                                                                                                                 Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 KXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 246843; CAA86893.1; -.
BMBL; 271408; CAA96014.1; -.
SGD; SO005076; YRL132w.
Hypothetical protein; ATP-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90221913; PubMed=2183201;
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96109932; PubMed=8619318;
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                                                                                                          34, Created)
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nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                          01-OCT-1996
                                                                  YNN2_YEAST
P53914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y9K_BPP4
P12552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                           YNN2_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98037514; PubMed=9371463;
A Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gibbert K., Aldredge T., Bashirzadeh P., Lumm W., Pothier B., Qiu D., Aldredge T., Bashirzadeh P., Wierzbowski J., Gibson R., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Andredge R., Shimer G., Goyal A., Patroeli D., Prabhakar S., McDougall S., Shimer G., Goyal A., Peterovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).

-I PROKITON: DNA REPARK EMZYME THAT INCISES DNA AT 8-OXG RESIDUES. EXCISES 7.8-DIMYDRO-8-OXGUANINE AND 2.6-DIAMINO-4-HYDROXY-5-N-METHYLPORMAMIDOPRIMIDINE (FRPY) FROM DAMAGED DNA. HAS A BETALYREORMAMIDOPRIMIDINE (FRPY) FROM DAMAGED DNA. HAS A BETALYREORMAMIDOPRIMIDINE (FRPY) FROM DAMAGED UNA. HAS A BETALYREORMAMIDOPRIMIDINE (FRPY) FROM DAMAGED ONA. HAS A BETALYREORMAMIDOPRIMIDINE (FRPY) FROM Cleavage near apurinic or apyrimidinic sites to products with 5'-phosphate.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
91ycosylase/DNA.lyase [Includes: 8-oxoguanine DNA glycosylase (EC 3.2.2.); DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP lyase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRPAMS; TIGR00588; ogg; 1.
Hydrolase; Nuclease; Endonuclease; Lyase; DNA repair; Glycosidase;
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                  LEWLRXXXXXXXXXXLLXXXGXGLKSXECVRLLXLXX-XAFPVDTNVGRIXVR 127
                                                                                                                                                                                                                                                                                                                                                                                     Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 312;
30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D33B4FF497BC5A1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLXXXGXGLKSXECVRLLXL-XXXAFPVDTNVGRI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 LLELSGVGPKVADCILLYGFRKTEAFPVDVWIRRI 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.1;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multifunctional enzyme; Complete proteome. ACT_SITE 235 235 BY SIMILARITY
                                                                                                                                                                                               312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000897; AAB85820.1; -.
InterPro; 1PR003265; Endo_3c.
InterPro; 1PR004583; HHH_1.
InterPro; 1PR004577; Ogg.
Fam; PR00730; HHH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36051 MW;
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Matches 14; Conservative
Conservative
                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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16;
                                                                                                                                                                                               OGG1_METTH
O27397;
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Indels

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Mailing C., Calendar R., Christie G.E., Dale E.C., Debo G., Finkel S., Flensburg J., Ghisotti D., Kahn M.L., Lane K.B., Lin C.-S., Lindqvist E.H., Plerson L.S., Six E.W., Sunshine M.G., Ziermann R.; "DNA sequence of satellite bacteriophage P4."; Nucleic Acids Res. 18:1649-1649(1990).
                                                                                                                                                                                                                                                                                                             01-0cT-1989 (Rel. 12, Created)
01-0cT-1989 (Rel. 12, Last sequence update)
01-0cT-1994 (Rel. 30, Last annotation update)
Hypothetical 9.7 kDa protein (ORF88) (Putative DNA-binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae; unclassified Myoviridae.
NCBI_TaxID=10680;
703 KTLPPLLIKLSEQPPHYLHYLGVSYGLTQSLHKFWKNNSFVPV 745
                                                                                                                                                                                                                                        88 A.A.
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91

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SEQUENCE FROM N.A. (ISOFORM 1A).
MEDLINE-98012228; PubMed-9348312;
Kuo F.C., Sklar J.L.;
*Augmented expression of a human gene for 8-oxoguanine DNA glycosylase (MutM) in B lymphocytes of the dark zone in lymph node germinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boiteux S., Radicella J.P.; "The human OGG1 gene: structure, functions, and its implication in the process of carcinogenesis.";
             yeast OGG1 gene that is involved in ^{\prime\prime}_{,,}
                                                                                                                                                                                                                              "Opposite base-dependent reactions of a human base excision repair enzyme on DNA containing 7,8-dihydro-8-oxoguanine and abasic sites."; EMBO J. 16:6314-6322(1997).
Morishita K., Shinmura K., Kohno T., Taniwaki M., Ohwada S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-99250167; PubMed-10233168;
Mishioka K., Ohtsubo T., Oda H., Fujiwara T., Kang D., Sugimachi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *Expression and differential intracellular localization of two major forms of human 8-Oxoguanine DNA glycosylase encoded by alternatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99428653; PubMed-10497264; Dherin C., Radicella J.P., Dizdaroglu M., Boiteux S.; Excision of oxidatively damaged DNA bases by the human alpha-hOggl protein and the Polymorphic alpha-hOggl(Ser326Cys) protein which is frequently found in human populations.";
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1A).

Dhenaut A., Bolteux S., Radicella J.;
Genomic structure and promoter characterization of the human 8-OH-
guantine glycosylase gene (OGG1) gene.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chevillard S., Radicella J.P., Levalois C., Lebeau J., Poupon M.F., Oudard S., Dutrillaux B., Boiteux S.; "Mutations in OGG1, a gene involved in the repair of oxidative DNA damage, are found in human lung and kidney tumours.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shinmura K., Kohno T., Kasai H., Koda K., Sugimura H., Yokota J., "Infrequent mutations of the hOGG1 gene, that is involved in the excision of 8-hydroxyguanine in damaged DNA, in human gastric
                                                                                                                                                                                                          Bjoras M., Luna L., Johnsen B.E., Hoff E., Haug T., Rognes T.,
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-99380087; PubMed-10449904;
Bidda T., Hippo Y., Nakahori Y., Matsushita I., Kodama T.,
Nishimura S., Aburatani H.;
"Structure and chromosome location of human OGG1.";
Cytogenet. Cell Genet. 85:232-236(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arch. Biochem. Biophys. 377:1-8(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jpn. J. Cancer Res. 89:825-828(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION OF VARIANT CYS-326.
                       "Cloning of a human homolog of the the repair of oxidative DNA damage. Oncogene 14:2857-2861(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Biol. Cell 10:1637-1652(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20239648; PubMed-10775435;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98324718; PubMed-9662341;
                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1A).
MEDLINE-98026907; Pubmed-9321410;
                                                                                                                                                       J. Exp. Med. 186:1547-1556(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncogene 16:3083-3086(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spliced OGG1 mRNAs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT HIS-154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT GLN-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakabeppu Y.;
                                                                                                                                                                                                                        Seeberg E.;
            Yokota J.;
                                                                                                                                            centers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multifunctional enzyme; Nuclear protein; Mitochondrion;
Alternative splicing; Polymorphism.
ACT_SITE 249 249 BY SIMILARITY.
VARSPLIC 317 345 VLESADLRQSRHAQEPPAKRRKGSKGPEG -> VSVPRCPP (IN ISOPORM 1B).
VARSPLIC 317 345 VLESADLRQSRHAQEPPAKRRKGSKGPEG -> TPPSYRCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPFPTSLSPSPPSLMLGRGLPVTTSKARHPQIKQSVCTTRWGGGY (IN ISOFORM 1C).
VLFSADLRQSRHAQEPPAKRRKGSKGPEG -> GLLGNAFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHQLLRPLIFCQDHLREGPPIGRGDSQGEELEPQLPSSLSS
IPYGRCDHCWTKDVDDPDLYTHPSPGSRDGHTWTQAMPYKVV
SPLATVIGHVMQASLLAL (IN ISOFORM 2A).
VADCICLMALDRPQAVPUDVHWHIAQRDYSWHPTTSOAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVPTCANPAMLRSHQQSAERVPKGRKARWGTLDKEIPQAPS
                                                           CHARACTERIZATION OF VARIANTS GLN-46; HIS-154 AND CYS-326.
MEDLINE-20368626; PubMed=10908322;
Audebert M., Radicella J.P., Dizdaroglu M.;
Listante Specificity of the OGG1 gene found in human tumors on the substrate specificity of the OGG1 gene found in human tumors on the substrate specificity of the OGG1 gene found in human tumors on the substrate specificity of the OGG1 gene found in human tumors on the substrate specificity of the OGG1 gene found in human tumors on the substrate specificity of the OGG1 gene found in human tumors on the substrate Specificity of the OGG1 gene found in human tumors on FUNCTION: DNA REPAIR ENZYME THAT NICKS BORD.

LYAGE ACTIVITY THAT NICKS DNA 3' TO THE LESION.

-I-CATALYTIC ACTIVITY: Endonucleolytic cleavage near apurinic or apyrimidinic sites to products with 5'-phosphate.

-I-SOBCELLULAR LOCATION: NUCLEAR (ISOFORM 1A) AND MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISOFORM 2A).

**ATERNATIVE PRODUCTS: 8 ISOFORMS; 1A/ALPHA (SHOWN HERE), 1B, 1C, 2A/BETA, 2B, 2C, 2D AND 2E; ARE PRODUCED BY ALTERNATIVE SPLICING. 1A IS THE PREVALENT FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfan; PF00730; HhH-GPD; 1.
TIGREAMS; TIGRO0588; ogg; 1.
Hydrolase; Nuclease; Endonuclease; Lyase; DNA repair; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: UBIQUITOUS.
DISEASE: DEFECTS IN OGG1 ARE ASSOCIATED WITH TUMOR FORMATION.
SIMILARITY: BELONGS TO THE OGG1 FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 345;
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Pred. No. 0.57;
Nucleic Acids Res. 27:4001-4007(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, U96710; AAB81132.1; EMBL, Y11838; CAA72536.1; EMBL, Y11731; CAA72414.1; EMBL, AB000410; BAA19103.1; EMBL, AF003995; AAB61340.1; EMBL, U88527; AAB68614.1; EMBL, Y13277; CAA73726.1; EMBL, X13277; CAA73726.1; EMBL, AF026691; AA84013.1; EMBL, AJ131341; CAA10351.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M8620; AAB68614.1;

108620; AAB68614.1;

118277; CAA73726.1;

APC26691; AAB64013.1;

AJ131341; CAA10351.1;

APC88282; AAD41680.1;

APC88282; AAD41680.1;

APC88282; AAD41680.1;

APC88282; AAD41680.1;

APC88282; AAD41680.1;

ABC19528; BAA76635.1;

ABC19539; BAA76636.1;

ABC19531; BAA76638.1;

ABC19531; BAA76638.1;

ABC19531; BAA76638.1;
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InterPro; IPR004577; Ogg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345
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EMBL;
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EMBL;
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EMBL;
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4

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Query Match
Best Local (
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                                                96
                         Matches
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                                                                                                                                                                RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                    STRAIN-IT2 / SGSC1412 / ATCC 700720;
STRAIN-IT2 / SGSC1412 / ATCC 700720;
STRAIN-IT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; Pubmed-1167609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Mouyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R.K.;
Waterston R. Wilson R.K.;
Waterston R. Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: ADENINE GLYCOSYLASE ACTIVE ON G-A AND C-A MISPAIRS.
-i- COFACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE CATALYTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER POSITIONING OF THE BUZYME ALONG THE DNA STRAND (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRON-SULFUR (4FE-45) (BY SIMILARITY).
IRON-SULFUR (4FE-45) (BY SIMILARITY).
IRON-SULFUR (4FE-45) (BY SIMILARITY).
IRON-SULFUR (4FE-45) (BY SIMILARITY).
SCS5DB4D7B7BB69F CRC64;
                                                                                                                                                                                                                        Desiraju V., Shanabruch W.G., Lu A.L.;
"Nucleotide sequence of the Salmonella typhimurium mutB gene, the homolog of Escherichia coli mutY.";
J. Bacteriol. 175:541-543(1993).
                                                                                                                          Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
PROSITE; PS01155; ENDONUCLEASE_III_2; 1.
DNA repair; Hydrolase; Glycosidase; Iron-sulfur; 4Fe-4S;
                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
AG-Specific adenine glycosylase (EC 3.2.2.-).
MUTY OR MUTB OR STM3110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AE008843, AAL21985.1; ---
PIR; A40647; A40647.
HSSP: P17802; JMON.
StyGene; SG10238; mutY.
InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR004036; EndoIII_HH.
InterPro; IPR003265; EndoIII_HH.
InterPro; IPR003583; HHH_1.
Fam; PF00730; HHH-GPD; IPR003783; HHH_1.
SMART; SM00478; ENDO36; 1.
                                                                                                                                                                                                               MEDLINE-93123173; PubMed-8419300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39409 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIGRFAMS; TIGR01084; mutY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 413:852-856(2001)
                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192
199
202
208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00278; HhH1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192
199
202
208
350 AA;
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
                                                                                                                                                               NCBI_TaxID=602;
                                                                                                                                                                                                     STRAIN-GW1803;
                                  MUTY_SALTY
Q05869;
                                                                                                                                                     Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
SEQUENCE
                       MUTY_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
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           RESULT 9
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SEQUENCE FROM N.A. (ISOFORM 2).
MEDILINE-9738611; Pubmed-9223306;
ROldan-Arijona T., Wei Y.-F., Carter K.C., Klungland A., Anselmino C.,
Wang R.-P., Augustus M., Lindahl T.;
"Molecular cloning and functional expression of a human cDNA encoding
the antimutator enzyme Bhydroxyguanine-DNA glycosylase.";
proc. Natl. Acad. Sci. U.S.A. 94:8016-8020(1997).
                                                                                                                                             GXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLXXXQXHXLXXYPXXXXXQ 155
                                                                                                                                                                                                               GVGRSTAGAILSLALGKHYPILDGNVKRVLAR------------CYAVSGWPGKKEVE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aburatani H., Hippo Y., Ishida T., Takashima R., Matsuba C., Kodama T., Takao M., Yasui A., Yamamoto K., Asano M., Fukasawa K., Yoshinari T., Inoue H., Otsuka E., Nishimura S.; "Cloning and characterization of mammalian 8-hydroxyguanine-specific homologue.";
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Radicella J.P., Dherin C., Desmaze C., Fox M.S., Boiteux S.; "Cloning and characterization of hOGG1, a human homolog of the OGG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OGGI_HUMAN STANDARD; PRT; 345 AA.
OGGI_HUMAN STANDARD; PRT; 345 AA.
O15527; O00390; P78554; O00670; O00705; O14876; O95488; Q9UL34;
O15527; O00390; P78554; O00670; O00705; O14876; O972C1;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
N-91ycosylase/DNA lyase [Includes: 8-oxoguanine DNA glycosylase (EC 3.2.2.-); DNA-(apurinic or apyrimidinic site) lyase
OGGI OR MMH OR MUTM OR OGHI.
                                                                        34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A mammalian DNA repair enzyme that excises oxidatively damaged guanines maps to a locus frequently lost in lung cancer."; Curr. Biol. 7:397-407(1997).
                                                                                                                                                                                                                                                                                       156 KXLWPRLCKLXQXTLYE------LHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                         162 NTLW-----TLSEQVTPARGVERFNQAMMDLG-AMVCTRSKPKCTLCPL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1A).
MEDLINE=97352815; PubMed=9207108;
ROSENQUIST T.A., Jahrkov D.O., Grollman A.P.;
"Cloning and characterization of a mammalian 8-oxoguanine DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Length 350;
                                                                        45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene of Saccharomyces cerevisiae.";
proc. Natl. Acad. Sci. U.S.A. 94:8010-8015(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 94:7429-7434(1997)
   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                       0.33;
                                                                        12; Mismatches
       Score 55;
                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [5]
SEQUENCE FROM N.A. (ISOFORM 1A).
MEDLINE-97342862; PubMed-9197244;
Lu R., Nash H.M., Verdine G.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97330655; PubMed=9187114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1A).
MEDLINE=97368310; PubMed=9223305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [6]
SEQUENCE FROM N.A. (ISOFORM 1A).
MEDLINE-97334205; PubMed-9190902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cancer Res. 57:2151-2156(1997).
   7.98;
19.58;
                                                                        22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycosylase.";
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us-09-840-743-72.rsp

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TISSUE=Lung;
MEDLINE=98026907; PubMed=9321410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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    NA RABARARA RABARA RABA
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                                                                                                                                                                                               AP LYASE ACTIVITY.
K->R: DIMINISHES BOTH DNA GLYCOSYLASE AND
AP LYASE ACTIVITY.
                                                                                                                                                                               K->Q: ABOLISHES BOTH DNA GLYCOSYLASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=97330655; Pubmed=9187114;
Aburatani H., Hippo Y., Ishida T., Takashima R., Matsuba C.,
Kodama T., Takao M., Yasul A., Yamamoto K., Asano M., Fukasawa K.,
Yoshinari T., Inoue H., Otsuka E., Nishimura S.;
"Cloning and characterization of mammalian B-rydroxyguanine-specific
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                    Pfam; PF00730; HNH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
TIGRPAMS; TIGR00588; ogg; 1.
Hydrolase; Nuclease; Endonuclease; Lyase; DNA repair; Glycosidase; Multifunctional enzyme; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OGGI_MOUSE STANDARD; PRT; 345 AA.
OGR160: 008991; 035915; 035617; 008733; 008910; 090XE8;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-CT-201 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97342862; PubMed-9197244;
Lu R., Nash H.M., Verdine G.L.;
"A mammalian DNA repair enzyme that excises oxidatively damaged
guanines maps to a locus frequently lost in lung cancer.";
Curr. Biol. 7:397-407(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ONA glycosylase/apurinic, apyrimidinic lyase, a functional mutM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97352815; PubMed-9207108; Rosenquist T.A., Zharkov D.O., Grollman A.P.; "Cloning and characterization of a mammalian 8-oxoguanine DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tani M., Shinmura K., Kohno T., Takenoshita S., Nagamachi Y., Yokota J.;
                                                                                                                                                                                                                                                                                                           DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                  4ADB72EB20E4BF20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 94:7429-7434(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                        91 LLXXXGXGLKSXECVRLLXLXXXAF-PVDTNVGRIXVR 127
                                                                                                                                                                                                                                                                                                         Score 56.5; DB Pred. No. 0.2; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98096582; PubMed=9434942;
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                                                                                                                                                                                                                                                                  376 AA; 42781 MW;
  IPR003265; Endo_3c.
                                                                                                                                                                                                                                                                                                         8.2%;
ilarity 39.5%;
Conservative
                                                                                                                                                                                                                      241
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es 15; Conserv
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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  InterPro;
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MUTAGEN
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                                   "Opposite base-dependent reactions of a human base excision repair enzyme on DNA containing 7,8-dihydro-8-oxoguanine and abasic sites."; EMBO J. 16:6314-6322(1997).
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                                                                                                                                                                                                                                                                                      Johnsen B., Luna L., Rognes T., Seeberg E.; "Complete genomic DNA sequence of the Mus musculus 8-oxoguanine DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Nuclease; Endonuclease; Lyase; DNA repair; Glycosidase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55.5; DB 1; Length 345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J;
Radicella J.P., Reille F., Dherin C., Boiteux S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75BB0DDB084E4947 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U86621; AAB68616.1; -. AF00069; AAB63151.1; -. AF0012916; AAB94512.1; -. AF012912; AAB94512.1; JOINED. AF012913; AAB94512.1; JOINED. AR012914; AAB94512.1; JOINED. AR012914; AAB94512.1; JOINED. AR012915; AAB94512.1; JOINED.
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EMBL; Y13479; CAA73883.
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MGD; MGI:1097693; Oggl.
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Best Local Similarity
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29;

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                                                                                                                                                                                      91 LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
                                                                                                                                                                                                                             - 144
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"Rat 7,8-dihydro-8-oxoguanine DNA 91ycosylase: substrate specificity,
kinetics and cleavagemechanism at an apurinic site.";
Nucleic Acids Res. 26:5199-5202(1998).
-!- FUNCTION: DNA REPAIR ENZYME THAT INCISES DNA AT 8-OXOG RESIDUES.
EXCISES 7.8-DIHYDRO-8-OXOGUANINE AND 2,6-DIAMINO-4-HYDROXY-5-N-
METHYLEORMAMIOPYRIMIDINE (FAPY) FROM DAMAGED DNA. HAS A BETA-
LYASE ACTIVITY THAT NICKS DNA 3' TO THE LESION.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage near apurinic or
apyrimidinic sites to products with 5'-phosphate.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                         Gaps
            SIMILARITY).
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SMART; SM00478; ENDO3c; 1.
TIGREAMs; TIGR00588; ogg; 1.
Hydrolase; Nuclease; Endonuclease; Lyase; DNA repair; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNY-2002 (Rel. 41, Last sequence update)
15-UNY-2002 (Rel. 41, Last annotation update)
N-glycosylase/DNA lyase [Includes: 8-Oxoguanine DNA glycosylase (RC 3-22.2.); DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.91)
                                                                                                                                                       31;
                                                                                                                                                                                                                                                         151 XXXXQKXLWPR-----LCKLXQXTLY-ELHYXXITFGKXXFCTKXXPNCNAC 196
                                                                                                                                                                                                                                                                                 ----KTRIPEETEEALKKLLPEDLWGPINGSMVEFGR-RICKPONPLCEEC 190
                                                                                                                     8.2%; Score 56.5; DB 1; Length 213; 25.0%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56.5; DB 1; Length 345; Pred. No. 0.18;
                                                                                                                                                       Indels
                                187 IRON-SULFUR (4FE-4S) (BY 190 IRON-SULFUR (4FE-4S) (BX 196 IRON-SULFUR (4FE-4S) (BX 24928 MW; D9716CD6FEFA85D4 CRC64;
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T_SITE 249 249 BY SIMILARITY.
QUENCE 345 AA; 38711 MW; B7FDF8C782644C41 CRC64;
Complete p (4FE-4S) (
                                                                                                                                                       45;
                                                                                                                                                                                                                      104 LLKLPGVGRKTANIVLWVGFKKPALAVDTHVHRISNRLGWV---
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            IRON-SULFUR (
IRON-SULFUR (
IRON-SULFUR (
IRON-SULFUR (
Iron-sulfur; 4Fe-4S;
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MEDLINE=99030527; PubMed=9801319;
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InterPro; IPR003265; Endo_3c.
InterPro; IPR004577; Ogg.
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                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                187
190
196
                              187
190
196
213 AA;
 Lyase;
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Best Local Similarity
Matches 28; Conserv
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Best Local Similarity
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SEQUENCE
                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97388538; PubMed-9241232;
Girard P.M., Guibourt N., Boiteux S.;
"The Ogg1 protein of Saccharomyces cerevisiae: a 7,8-dihydro-8-
oxoguanine DNA glycosylase/AP lyase whose lysine 241 is a critical
residue for cataly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION, AND MUTAGENESIS OF LYS-241.
MEDLINE=20143487; PubMed=10677220;
Guibourt N., Castaing B., Van Der Kemp P.A., Boiteux S.;
Catalytic and DNA binding properties of the ogg1 protein of
Saccharomyces cerevisiae: comparison between the wild type and the
K241R and K241Q active-site mutant proteins.";
Biochemistry 39:1716-1724(2000).
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SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE OGG1 FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         van der Kemp P.A., Thomas D., Barbey R., de Oliveira R., Boiteux "Cloning and expression in Escherichia coli of the OGG1 gene of Saccharomyces cerevisiae, which codes for a DNA glycosylase that excises 7,7 editydro-8-oxognanine and 2,6-diamino-4-hydroxy-5-N-methylfornamidopyrimidine.";
                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
N-glycosylase/DNA lyase [Includes: 8-oxoguanine DNA glycosylase (EC 3-2.2.); DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP lyase)].
0GG1 OR YML060W OR YM9958.02.
                                         76 LEWLRXXXXXXXXXXXXLXXXGXGLKSXECVRLLXLXX-XAFPVDTNVGRIXVR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Devlin K., Churcher C., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 93:5197-5202(1996)
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                                                                                                                                                                                                                                                               376 AA
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                                                                                                                                                                                                                                                                                                                                       (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U44855; AAC49312.1; -. EMBL; Z46729; CAA86715.1; -. SGD; S0004525; OGG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methylformamidopyrimidine.
                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                            01-OCT-1996
01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                                                       OGG1_YEAST
P53397;
                                                                                                                                                                                                                                                                   HDD BERNES BERNE
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us-09-840-743-72.rsp

Sat Nov

DB 1; Length 142;

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RA MEDIUME-12184/49; UnumAGG-11/80U32;

RA MEDIUME-22184/49; UnumAGG-11/80U32;

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Balley J., Baltow K.F., Bates K.N., Beard L.M., Beare D.M.,

RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

Clegg S., Cobley V.E., Collier R.E., Carder C., Carter N.P.,

Clegg S., Cobley V.E., Collier R.E., Compor R.E., Corby N.R.,

RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

RA Lington A.G., Frankland J.A., Frascr A., French L., Garner P.,

RA Grafham D.V., Griffiths C., Griffiths M.D., Gwilliam R., Hall R.E.,

RA Huckle E., Hunt A.R., Hunt S.E., McConnachie L.J., Moden P.J.,

RA Marsh V.L., Martin S.L., McConnachie L.J., Adhason C.M., Johnson D.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.R.,

RA Mine S.A., Mattry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Dillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,

RA Swance N., Taylor R., Thomas D.W., Thorpe A.,

RA Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

RA Wilting L., Witay P.W., Hubbard T., Durbin R.W., Bentley D.R., Williams S.A.,

RA Miner S.L., Wattaker P., Willey D.L., Williams L., Williams S.A.,

RA Swann R.W., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

RA Milling L., Wiray P.W., Hubbard T., Durbin R.W., Bentley D.R., Rapers J.,

RA Marer S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C -> R (IN 45% OF THE POPULATION).
/FTId=VAR_002208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYSTATIN D.
REACTIVE SITE (BY SIMILARITY).
SECONDARY AREA OF CONTACT.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CEFA89BA87A0DA68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Polymorphism.
 SEQUENCE FROM N.A.
MEDLINE-21638749; PubMed=11780052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X59964; CAA42590.1; -.
EMBL; X70377; CAA49838.1; -.
EMBL; ALS91074; CAC94785.1; -.
PIR; S18212; S18212.
HSSP; P01034; 1G96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000010; Cystatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00043; CY; 1.
PROSITE; PS00287; CYSTATIN; 1.
Thiol protease inhibitor; Sign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16080 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00031; cystatin; 1.
SMART; SM00043; CY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:2477; CST5.
MIM; 123858; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105
139
46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT ARG-46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rogers J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=WSB8 / DSW 3109;
MEDLINE=99287316; PubMed=10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
M. Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
M. Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Rividence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";
I syldence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";
I shift D.H., M. ADBOTH AN ADVINIT AND APWRED STRAND, S.
C. TONSINES, THYMINES AND GUANINES. ACTS ON A DAMAGED STRAND, 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003265; Endo_36.
InterPro; IPR003265; Endo_36.
InterPro; IPR003563; HHL_1.
InterPro; IPR003583; HHL_1.
Pfam; PF00730; Hhl-GPD; 1.
SMART; SM00478; ENDO36; 1.
SMART; SM00478; ENDS; 1.
SMART; SM00478; Hhll; 1.
INTERPAMS; TIGR01083; nth; 1.
TIGREAMS; TIGR01083; nth; 1.
PROSITE; PS001764; ENDONUCLEASE_III_1; 1.
Hydrolase; Nuclease; Endonuclease; Multifunctional enzyme; DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM THE DAMAGED SITE (BY SIMILARITY).

CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or apprinding tion reaction, apprinding site in DNA is broken by a beta-elimination reaction, leaving a 3'-terminal unsaturated sugar and a product with a terminal 5'-phosphate.

COPACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE CATALYTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER POSITIONING OF THE ENZYBE ALONG THE DAMA STRAND (BY SIMILARITY).
                                        Gaps
                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Endonuclease III (EC 4.2.99.18) (DNA-(apurinic or apyrimidinic site)
                                                                                                                                                                                                                                                                                                                                                                              Thermotoga maritima.
Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
Thermotogaceae; Thermotoga.
                                     Indels
Score 57.5; DB Pred. No. 0.052;
                                                                                                                                                                                                                      213 AA.
                                     4; Mismatches
                                                                             174 HYXXITFGKXXFCTKXXPNCNACP 197
                                                                                                       InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR004036; EndoIII_HhH.
InterPro; IPR003265; Endo_3c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001716; AAD35453.1; -. HSSP; P20625; 2ABK.
                                        10; Conservative
                                                                                                                                                                                                                      STANDARD;
            Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; TM0366;
                                                                                                                                                                                                                                                                                                                                                             NTH OR TM0366
                                                                                                                                                                                                                    END3_THEMA
O9WYK0;
  Query Match
                                                                                                                                                                                                                                                                                                                                              lyase)
                                                                                                                                                                                                   END3_THEMA
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                                                                                                                                                                              RESULT
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Biol. Chem. 268:15737-15744(1993)
                                                                                                                  Ecocene; EG10627; muty.
Interpro; IPR004036; EndoIII_FCL.
Interpro; IPR004036; EndoIII_HH.
Interpro; IPR003265; Endo_3c.
Interpro; IPR003561; Fee_bind.
Interpro; IPR003583; HHH_1.
Pfam; PF00730; HhH-GPD; 1.
SWART; SW00478; ED03c; 1.
SWART; SW00525; FES; 1.
              Li, AE000378; AAC75998.1; -. 00546; JQ0546.
1; B36535; B38535.
1; IMUD; 29-OCT-99.
1; IMUN; 26-AUG-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 AA; 39149 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cystatin D precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTD_HUMAN
P28325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTD_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
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                                                                                                                                                                                                                                                                                                                                                                                                              Michaels M.L., Pham L., Nghiem Y., Cruz C., Miller J.H., "MutY, an adenine glycosylase active on G-A mispairs, has homology to endonuclease III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LAKGNT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INVOLVED IN THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COFACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE CATALYTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER POSITIONING OF THE ENZYME ALONG THE DNA STRAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shoo Y.;
                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                     156 AAIVEKEL---LQIIDEKWLTYAHHWLILHGR-YICKARKPGCNICPI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsai-Wu J.-J., Radicella J.P., Lu A.-L.;
"Nucleotide sequence of the Escherichia coli micA gene re
A/G*specific mismatch repair: identity of micA and mutY."
J. Bacteriol. 173:1902-1910(1991).
111 LVKLPGVGRKTANVVLNCLFAMPTMAVDTHVFRVSKRIG----
                                                                                                                                                                                  01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
AUG-specific adenine glycosylase (EC 3.2.2.-).
MUTY OR MICA OR B2961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY
                                                                                                                                                      350 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 18:3841-3845(1990)
                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90326504; PubMed=2197596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91161503; PubMed=2001994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X52391; CAA36624.1; -. EMBL; M59471; AAA72957.1; -.
                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        Escherichia coli
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OXOGUANINE.
                                                                                                                  RESULT 3
MUTY_ECOLI
ID MUTY_ECOLI
AC P17802;
                                                                                                                                                                                                                                                                                                          Escherichia
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TIGREAMS; TIGRO1084; muty; 1.
PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
PROSITE; PS01155; ENDONUCLEASE_III_2; 1.
DNA repair; Hydrolase; Glycosidase; Iron-sulfur; 4Fe-4S; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93340179; PubMed=8340398; Ereije J.P., Balbin M., Abrahamson M., Velasco G., Dalboge H., Grubb A., Lopez-Otin C.; "Human cystatin D. c.; "Human cystatin D. coli expressed inhibitor, and identification of the native protein in saliva.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 GXGLKSXECVRLLXLXXXAFPV-DTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPXXXXX 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lopez-Otin C.; "Structure and expression of the gene encoding cystatin D, a novel human cysteine proteinase inhibitor."; U. Biol. Chem. 266:20538-20543(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=92041895; PubMed=1939105;
Freije J.P., Abrahamson M., Olafssonn I., Velasco G., Grubb A.,
                                                                                                                                                                                                                                                                                                                                                        8.5%; Score 59; DB 1; Length 350; 20.2%; Pred. No. 0.071;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                          C7D3657C03EBBF4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 ENKLWSLSEQVTPAVGVERFNQAMMDLGAMICTRSKPKCSLCPL 204
                                                                                                                                                             IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches
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3;

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Rickettsia prowazekii
                                             NCBI_TaxID=782;
                                                                                                                                                                                                                   STRAIN-Madrid
                                                                                                                                                                                                                                                                                                   mitochondria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                Nature 390:249-256(1997).
-!- CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or apyrimidinic site in DNA is broken by a beta-elimination reaction, leaving a 3'-terminal unsaturated sugar and a product with a terminal 5'-phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA repair;
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosako V., Uchiyama S., Vandehol M., Vannier F., Vassarotti A., Vlari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 LLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLPXXXQXHXLXXYPX 150
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                                                                                                                                                                    COFACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE CATALYTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER POSITIONING OF THE ENZYME ALONG THE DNA STRAND (BY SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Endonuclease III (EC 4.2.99.18) (DNA-(apurinic or apyrimidinic site)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS00764; ENDONUCLEASE_III_1; 1.
PROSITE: PS01155; ENDONUCLEASE_III_2; 1.
Hydrolase; Nuclease; Endonuclease; Multifunctional enzyme; DNA repa Glycosidase; Lyase; Iron-sulfur; 4Fe-45; Complete proteome.
METAL 189 189 IRON-SULFUR (4FE-45) (BY SIMILARITY).
METAL 199 199 IRON-SULFUR (4FE-45) (BY SIMILARITY).
METAL 205 105 IRON-SULFUR (4FE-45) (BY SIMILARITY).
METAL 205 205 IRON-SULFUR (4FE-45) (BY SIMILARITY).
SEQUENCE 219 AA; 25000 MW; C38C66DA7948BA40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 XXXXQKXLWPRLCKLXQXTLYELHYXXITFGKXXFCTKXXPNCNACPM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----KEDWS------VTHHRLIFFGR-YHCKAQSPRCAECPL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 64; DB 1;
Pred. No. 0.0068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 EMBL, L47709; AMB38457.1; -
EMBL, 299115; CAB14150.1; -
BASP; P20625; 2ABK.
Subtilist; BG10956; nth.
InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR004035; EndoIII_HH.
InterPro; IPR003265; EndoIII_HH.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003583; HHH_1.
SMART; SW00478; ENDO3c; 1.
SMART; SW00478; ENDO3c; 1.
SMART; SW00525; FES; 1.
FIGRPAMS; TIGR01083; nth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.2%;
                                                                                                                                                                                                                                                                                                                                                        EMBL; U11289; AAA80005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25; Conservative
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005956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- FUNCTION: HAS BOTH AN APURINIC AND/OR APYRIMIDINIC ENDONUCLEASE
ACTIVITY AND A DNA N-GIYCOSYLASE ACTIVITY. INCISES DAMAGED DNA AT
CYTOSINES, THYMINES AND GUANINES. ACTS ON A DAMAGED STRAND, 5'
FROM THE DAMAGED SITE (BY SIMILARITY).

--- CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or
apyrimidinic site in DNA is broken by a beta-elimination reaction,
leaving a 3'-terminal unsaturated sugar and a product with a
terminal 5'-phosphate.

--- COFACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE
CATALYTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER
POSITIONING OF THE ENTYME ALONG THE DNA STRAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
PROSITE; PS00155; ENDONUCLEASE_III_2; 1.
PROSITE; PS01155; ENDONUCLEASE_III_2; 1.
Hydrolase; Nuclease; Endonuclease; Multifunctional enzyme; DNA repair; Glycosidase; Lyase; Iron-sulfur; 4Fe-45; Complete proteome.

METAL 187 187 IRON-SULFUR (4FE-45) (BY SIMILARITY).

METAL 197 IRON-SULFUR (4FE-45) (BY SIMILARITY).

METAL 203 203 IRON-SULFUR (4FE-45) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andersson S.G.E., Zomorodipour A., Andersson J.O., sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                   Andersson J.O., Andersson S.G.E.; "Genomic rearrangements during evolution of the obligate intracellular parasite Rickettsia prowazekii as inferred from an analysis of 52015 bp nucleotide sequence."; Microbiology 143:2783-2795(1997).
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred No. 0.0079;
10; Mismatches 53; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99039499; PubMed-9823893;
                                                                                                                                                                                          STRAIN-Madrid E;
MEDLINE-97419517; PubMed-9274032;
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InterPro; IPR004036; EndoIII_HHH.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003651; Feg_bind.
InterPro; IPR003583; HHH_1.
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EMBL; AJ235273; CAA15174.1; -.
HSSP; P20625; 2ABK.
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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RESULT 1
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005956 rickettsia
P17802 escherichia
P28325 homo sapien
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homo sapien
methanobact
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schizosacch
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                                                                                                                                                                                                                                   arabis
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P28362
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                      112892 seqs, 41476328 residues
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END3_RICPR
MUTY_ECCLI
CYTD_HUMAN
END3_THEMA
OGG1_RAT
OGG1_XEAST
OGG1_NOUSE
MUTY_SALTY
OGG1_HUMAN
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YNN2_YEAST
YOK_BPP4
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MAKE_MOUSE
CYTC_SAISC
END3_TREPA
ETFA_HUMAN
ETFA_MOUSE
CUTI_CAEEL
MYH_SCHPO
YAO7_SCHPO
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MUTY_BUCAI
VP3_ARMV
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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P76269 escherichia	P01037 homo sapien	014359 schizosacch	Q9v3i8 drosophila	P58395 thermus cal	Q9z1t6 mus musculu	Q9qzt3 rattus norv	P16710 vaccinia vi	Q58030 methanococc			Q9yb79 aeropyrum p
YEBQ_ECOLI	CYTN_HUMAN	YB4E_SCHPO	OGG1_DROME	GLGA_THECA	FYV1_MOUSE	PA2X_RAT	VA16_VACCV	Y613_METJA	VA16_VARV	VA16_VACCC	GATB_AERPE
П	-	Н	Н	Ξ.	П	-	Н	7	Н	Н	Н
457	141	249	327	438	2052	151	275	344	377	378	486
9.9	6.5	6.4	6.4	6.4	6.4	6.3	6.3	6.3	6.3	6.3	6.3
45.5	45	44.5	44.5	44.5	44.5	44	44	44	44	44	44
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## ALIGNMENTS

END3_BACSU ID END3_BACSU STANDARD; PRT; 219 AA.		01-FEB-1995 (Rel. 31, Creat	DT 15-JUN-2002 (Rel. 31, Last sequence update) DT 15-JUN-2002 (Rel. 41, Last annotation update)	Probable endonuclease	DE apyrimidinic site) lyase). GN NTH OR JOOB.	Baci		OX NCBI_TaxID=1423; RN [1]			RX MEDLINE=95219085; PubMed=7704260; Pa Briand C Sorokin a Sorior D Fhrlich S D .	RT "Nucleotide sequence of the Bacillus subtilis dnaD gene.";	Microbiology 141:321-322(1995).		RP SEQUENCE FROM N.A.			Serror P.;	"Sequence analysis of the Bacillus subtilis chromos	KT the serA and kdg loci cloned in a yeast artificial chromosome."; RI. Microbiology 142:2005-2016/1996.		RP SEQUENCE FROM N.A.				KA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., PA Borries P. Boursier F. Brans A. Braun M. Brignell S.C. Bron S.		RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,		Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,	rk . Filtz C., Fujita M., Fujita I., Fuma S., Galizzi A., Galieron N., RA Ghim S.Y., Glaser P., Goffean A., Golichtly E.J., Grandi G.				KA KODAYASNI Y., KOETTET P., KONINGSTEIN G., KIOGN S., KUMANO M., RA Kurita K Tanidus A Tandinois S Tamber T Tazarevio V		Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noba	RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,	Parico V., Polli I.M., Policecalle D., Polwollik S., Frescott A.M., Dracers Draces Division D		Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,	ta A., Seror S.J., Serror P., Shin B.S.	COLONIE A., INCCOLL E., INVAGE I., INVALIGABLE II.,	
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2374 2472 CADHERIN 22.
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2807 3020 CADHERIN 26.
1070 1070 I -> V (IN REF. 3).
1490 1490 S -> R (IN REF. 3).
1636 1636 S -> R (IN REF. 3).
1636 1692 P -> S (IN REF. 3).
1602 2029 1 -> V (IN REF. 3).
2209 2029 I -> V (IN REF. 3).
2210 A -> P (IN REF. 3).
2269 2289 C -> P (IN REF. 3).
2362 2536 T -> S (IN REF. 3).
2363 2338 3038 G -> R (IN REF. 3).
3503 AA: 379721 MW; F256924D5FB5F7AE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-EMBRYO;
MEDLINE-95324813; PubMed-7601355;
MEDLINE-95324813; PubMed-7601355;
Clark H.F., Brentrup D., Schneitz K., Bieber A., Goodman C., Noll M.;
"Dachsous encodes a member of the cadherin superfamily that controls imaginal disc morphogenesis in Drosophila.";
Genes Dev. 9:1530-1542(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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                                                                                       "Genome sequence of the nematode C.elegans: A platform for
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                                Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                         DNA binding; Zinc-finger.
SEQUENCE 624 AA; 71971 MW; 39E9BD2838A9C8D3 CRC64;
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Last annotation update)
                                                                                                 investigating biology.";
Science 283:2012-2018(1998).
EMBL, 27552; CAA99942.1;
InterPro; IPRO00822; Znf_C2H2.
Pfam; PF00096; zf_C2H2; ZnF_C2H2; ZnFCZH2; ZnF_CZH2; IPROSTTE; PS00028; ZINC_FINGER_CZH2, I.
PROSTTE; PS50157; ZINC_FINGER_CZH2, I.
PROSTTE; PS50157; ZINC_FINGER_CZH2, I.
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64.3%; Pred. No. 23;
iive 0; Mismatches
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                                                                   MEDLINE=99069613; PubMed=9851916;
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01-NOV-1996 (TrEMBLrel. 01,
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les 9; Conservative
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-!- FUNCTION: INVOLVED IN MORPHOGENESIS. MAY ALSO BE INVOLVED IN CELL
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-!- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC ECTODERM. IN LARVAE,
EXPRESSION IS RESTRICTED TO IMAGINAL DISKS AND BRAIN.
-!- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT EMBRYOGENESIS WHERE IT
IS FIRST DETECTED DURING GASTRULATION. ALSO EXPRESSED IN LARVAE
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PROSITE; PS50268; CADHERIN_2; 27.
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
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DACHSOUS PROTEIN.
EXTRACELLULAR (POTENTIAL).
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InterPro; IPR002637; Hamlp_like.
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                          Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium NCBL_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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Pfam; PF0550; pp-binding; 1.
PROSTIE; PS06075; ACP_DOMAIN; 1.
PROSTIE; PS06065; B_KETOACYL_SYNTHASE; 1.
PROSPIDEDAULELHEINE; Transferase; Complete proteome.
SEQUENCE 1540 AA; 164209 MW; D7042CAAREED72375 CRC64;
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               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                          Murphy L., Harris D.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein R00374.
                                                                                                                                                                                                                                                                 "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011/2001).
BELS ALO35480; CAB36627 11; --
EMBL; ALO35925; CAC31872.1; --
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InterPro, IPR000794; Ketoacyl.synt.
InterPro, IPR003880; Ppantne_attach.
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MEDLINE=21396507; PubMed=11481430;
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Pfam; DE00001: '--
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Best Local Similarity 30.4.
8; Conservative
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Mycobacterium leprae.
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NCBI_TaxID=6239;
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                Length 214;
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006625; AAK68271.1; -.
SEQUENCE 325 AA; 37141 MW; 55EAA4186BC645C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The sequence of C. elegans cosmid C55B7.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
Pfam; PF01725; Hamlp_like; 1.
TIGREMS; TIGR00042; Hamlp_like; 2.
Hypothetical protein; Complete proteome.
SEQUENCE 214 AA; 23109 MW; A282C7539C9BGDD CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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                                                                                                            Score 37; DB 16;
Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                      110 RTEHXVXXL----PDXHXXLXXXDXXXYLLXIWXP 140
                                                                                                                                                                                                                                    125 RTARFVSVLCLAWPDGHVELFRGEVEGYV--VWPP 157
                                                                                                                                                                                                                                                                                                                                                                325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           624 AA
                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.3%; Score 37; DB
86.0%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 LRTEHXVXXLPDXHXXLXXXXXXX 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 INTETLIEILPDGKLILNPRDASKY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein C55B7,11.
                                                                                                              6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01,
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20,
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W04D2.4.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel
01-DEC-2001 (TrEMBLrel
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF408195; AAL05551.1; -.
InterPro; IPR002934; NTP_transf.
Pfam; PF01909; NTP_transf.2; 1.
Plasmid; Transferase.
SEQUENCE 242 AA; 27360 MW; 503A1E863E48B90C CRC64:
                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Q9S384
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Q49932
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell W., Honderson S.N.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brail J.F., Apbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Burils R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Antilon D.,
Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Antilon D.,
RA Burils K.C., Blasm D.A., Butler H.-, Cadleu E., Conter A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H.-, Cadleu E., Conter A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Conter A., Chandra I.,
RA Cavley S., Dahke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
Chodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,
RA Gebbricklan A.E., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Andris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Andrin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Hinton G.S., Pan S., Pollard J., Worther S., Shen H.,
Rheinert K., Mathor R.B., Murphy L., Murahy D.M., Nelson D.L.,
RA Balazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,
Shee B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
The genome sequence of Drosphila melanogaster.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gentry-Weeks C.R., Keith J.M., Estay M.T., Pikis A.;
Gentry-Weeks C.R., Keith J.M., Estay M.T., Pikis A.;
"A resident plasmid of Enterococcus faecalis 418 contains multiple
IS1216v elements, aminoglycoside and lincosamide resistance genes, and
a putative ABC transporter gene with similarity to the Streptococcus
pneumoniae macrolide efflux pump gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01501; Glyco_transf_8; 1.
SEQUENCE 1548 AA; 174352 MW; 87D782E7B27E0EE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              935 PRQTKTRFKLPTDLKTDHSVVKLPPKQENLPHFDVAAVL 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 PXXXXXXXXXXXXXRTEHXVXXLPDXHXXLXXXXXXXI 134
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Plasmid pEF418.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putative spectinomycin adenyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 6.9%;
Best Local Similarity 28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE003519; AAF49220:1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0014075; Ugt.
InterPro; IPR002495; GT_8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
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Robison K., Smith D.R.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION. FOTENTIALLY INVOLVED IN SOME INTERMEDIATE STEPS FOR THE SYNTHESIS OF A POLYKETIDE MOLECULE WHICH MAY BE INVOLVED IN SECONDARY METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibiotic biosyntness, nace, Ligase, Multifunctional enzyme; Repeat; Ligase, ACT_SITE 204 BETA-KETOACYL SYNTHASE (BY SIMILARITY).

ACT_SITE 651 ACYL TRANSFRASES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: TO FATTY ACID SYNTHASE (FAS).
-!- SIMILARITY: TO ENZYMES WHICH ACT VIA AN ATP-DEPENDENT COVALENT
BINDING OF AMP TO THEIR SUBSTRATE.

EMBL, 000023; AAA17356.1; -.
InterPro; IPR001227; Ac_transferase.
InterPro; IPR001294; Ketoacyl.synt.
Pfam; PF00699; Acv1_transf; 1.
Pfam; PF00699; Acv1_transf; 1.
Pfam; PF00609; Ketoacyl-synt; 1.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
Antibictic biosynthesis; NADP; Phosphopantetheine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: CONTAINS THREE COVALENTLY BOUND PHOSPHOPANTETHEINES
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6.4%; Score 38; DB 2; Length 242; 34.6%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Indels
                                                         Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
101-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative polyketide synthase.
ML2356 OR MLCB12.01C.
                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 20, Last annotation update)
                                                         16;
                                                                                                                                                                                                                                                                                               PRT; 1446 AA.
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                              Pred. No. 4.8;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                  Putative polyketide synthase PKSC (PKS).
PKSC OR L518_F1_2.
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                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                             109 LRTEHXVXXLPDXHXXLXXXDXXXYL 134
                                                                                                                                           990 DHDVSTLHDLHNALRGVDNVLY 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 EHXVXXLPDXHXXLXXXDXXXY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.48;
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Matches 8; Conservative
                                                         Conservative
                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium leprae.
                                Best Local Similarity
Matches 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 6.1 Kba protein (Fragment).
Narcissus pseudonarcissus (Daffodil).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 106.3 kDa protein.
F28A23.180 OR AT4G34060.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiphantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Weichselgartner M., Fartmann B., Granderath K., Dauner D., Herzl A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dauner D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bevan M., Weichselgartner M., Fartmann B., Granderath K., Herzl A., Neumann S., Hohelsel J., Jesse T., Heijnen L., V Mewes H.W., Mayer K., Schueller C.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL021961; CAA17566.1;
EMBL, AL161984; CAB80123.1;
InterPro; IPR003265; Endo_3c.
InterPro; IPR003651; FeS_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      il protein.
917 AA; 106310 MW; 302B3770ACE1A454 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 KXXXXLRTEHXVXXLPDXHXXL-----XXXDXXXYLLXIWXP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              836 KYYNRLRTEHVVYVLPDNHELLHDFERRKLDDPSPYLLAIWQP 878
                                                                                                                                                                                                                                                     049498;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.1%; Score 77; DB 10; 44.2%; Pred. No. 2.5e-08;
                                                                                                                1151 -IFQANGMLCDEETCFSCNSIKETRSQIVRGTIL 1183
                                                                                                                                                                                                                                    AA
                                                                  53 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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STRAIN=CV. DUTCH MASTER; TISSUE=TEPAL;
Hunter D.A., Reid M.S.;
                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00478; ENDO3c; 1.
SMART; SM00525; FES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00730; HhH-GPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Narcissus.
NCBI_TaxID=39639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
98 WWG
1D 08 WW
AC 08 WW
DT 01 - WM
DT 01 - WM
DE HYPO1
OS NATC:
OC BURAI
OC SPERT
OC SPERT
OC NATC:
OC NATC:
OC NATC:
OC NATC:
OC SPERT
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Goralez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AV058353, AAL13582.1; -.
FIYBase, FBGn0014075; Ugt.
SEQUENCE 1064 AA; 119309 MW; 40A569D1A68513CD CRC64;
"Identification of genes associated with perianth senescence in daffodil (Narcissus pseudonarcissus L. 'Dutch Master')."; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF402201; AAL6934.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                  0;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 1064;
                                                                                                                                                                                                                           Score 47; DB 10; Length 53;
Pred. No. 0.0083;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                 1FDE4BC8CED27346 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                3 IFKGLTTEGIQHCFWRGFVCVRGFDRMMRAPKPLFARLHFPASK 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 935 PRQTKTRFKLPTDLKTDHSVVKLPPRQENLPHFDVAAVL 973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1064 AA
                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1548 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                              8.0%;
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28.28;
                                                                                                                                                                               53 AA; 6138 MW;
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                                                                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 28.2
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                53
                                                                                                                                                                                                                                                          Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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OR CG6850.
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                                                                                                                                                                                 SEQUENCE
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Length 1309;

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SEQUENCE FROM N.A.
STRAING-CV. COLUMBIA;
MEDLINE-20083487; Pubwed-10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., Vanaken S.E., Unayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Niterman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                1109 KIKEKLRTEHHVFELPDHHSILEGFERREAEDIVPYLLAIWTP-GETVNSIQPPKQRC-- 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                     1166 ALFESNNTLCNENKCFQCNKTREEESQTVRGTILIPCRTAMRGGFPLNGTYFQTNEVFAD 1225
                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fuji C.Y., Utterback T.R., Barnstead M.E.
Bowman C.L., White O., Nlerman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC T22X18 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HDSSINPIDVPTELIWDLKRRVAYLGSSVSSICKGLSVEAIKYNFQEG 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56; Indels
                                                                                                                                                  Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
SMART; SM00525; FES; 1.
SEQUENCE 1309 AA; 148451 MW; 3B21E4439BA4A673 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDB6C9EE94DDF67 CRC64;
                                                                        Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AC010927; ARF04422.1; -. InterPro; IPR003265; Endo.3c. InterPro; IPR003651; FeS_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                             18.4%; Score 108.5; DB 10; 25.0%; Pred. No. 2.3e-15; ive 0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.4%; Score 91; DB 10; 29.8%; Pred. No. 2.1e-11; ive 0; Mismatches 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                      Conservative
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Submitted (MAR-2000)
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                                                                                                                                                                                                                                                                  Similarity
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NCBL_TaxID=3702;
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SEQUENCE 1207
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Q9SJQ6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 KNVSRLRTEHQVYELPDSHPLLEGFNQREPDDPCPYLLSIWTP-GETAQSTDAPKSVC-- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 -NSQENGELCASNTCFSCNSIREAQAQKVRGTLLIPCRTAMRGSFPLNGTYFQVNEVFAD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 HDSSRNPIDVPRSWIWNLPRRTVYFGTSIPTIFKGLTTEEIQHCFWRGFVCVRGFDRTSR 242
                                     154 HESSLKPIDVPRDWIWDLPRRTVYFGTSVTSIFRGLSTEQIQFCFWKGFVCVRGFEQKTR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 KXXXXLRTEHXVXXLPDXHXXLXX-----XDXXXYLLXIWXPXXXXXXXXXXXXXXX 157
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                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0665D10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.6%; Score 145; DB 10; Length 274; larity 26.2%; Pred. No. 2e-24; Conservative 0; Mismatches 134; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002861; BAB16489.1; -. SEQUENCE 274 AA; 30951 MW; D7C826BD3982592D CRC64;
                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                  274 AA
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                                                                                                                                                                                                                                                                                      Created)
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(TrEMBLrel. 16, I
(TrEMBLrel. 16, I
                                                                                                                                       1 1 11 214 APRPLMARLHFPASK 228
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                                                                                                             278 XPXXLXXXLHXXXSK 292
                                                                                                                                                                                                                                                PRELIMINARY;
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01-MAR-2001 (TrEMBLre)
P0665D10.14 protein.
P0665D10.14.
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STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                    01-MAR-2001
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Length 1207;

Qavc4 vallisneria Q9k3x3 streptomyce Q9alp2 saccharopol Q9a7u8 caulobacter Q9nvn5 homo sapien Q96cg1 homo sapien

093955 yarrowia li Q8zjkl yersinia pe Q9pj45 campylobact Q97v74 sulfolobus

O9vwc0 drosophila O99km7 mus musculu O51815 bacillus su

O9hzm8 pseudomonas Oguvn5 alternaria 005516 bacillus su

Q9pth9

09jsr4 neisseria m 09a7u3 caulobacter 007561 bacillus su 09hv38 pseudomonas 09rt59 deinococcus 08ycz9 brucella me

Q9abp5 caulobacter

Q8szx4 drosophila Q9vcz9 drosophila

Q9k164 neisseria m Q922g0 mus musculu

Sednence:

Run on:

Searched:

Database

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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Surosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 KXXXXLRTEHXVXXLPDXHXXLXXXDX-----XXYLLXIWXPXXXXXXXXXXXXXXXX 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W. Rudd S., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.7%; Score 146; DB 10; Length 234; 26.2%; Pred. No. 9.9e-25; Live 0; Mismatches 134; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL162875; CAB85564.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 234 AA; 26649 MW; B395392E066EB297 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 26.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                           Q9UVN5
005516
                                                                                                                                                                                                        Q9ALP2
Q9A7U8
Q9NVN5
Q96CQ1
Q922G0
                                                                      093955
Q8ZJK1
Q9PJ45
Q97V74
Q9VWC0
Q99KM7
                                                                                                                                                              O51815
Q9AVC4
Q9K3X3
                                                                                                                                                                                                                                                                                09K164
09JSR4
09A7U3
007561
09HV38
09KT59
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Q9ABP5
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les 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9LZ67
Q9LZ67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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Q9LZ67
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09ftq2 oryza sativ
09sr66 arabidopsis
09si6 arabidopsis
049498 arabidopsis
049498 arabidopsis
089wu6 narcissus p
09vu7 drosophila
09vu7 drosophila
099x47 mycobacteri
09s84 mycobacteri
09s84 rhizobium m
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024292 drosophila
029807 archaeoglob
                                                                                                              (without alignments)
1659.222 Million cell updates/sec
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                                                                                                  Search time 36.2614 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                       671580
         GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                             671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                  2002, 19:24:15
                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     protein search, using sw model
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Q9SR66
Q9SJQ6
049498
Q8VWU6
Q95U28
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sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
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sp_bacteria:*
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sp_plant:*
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sp_human:*
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Match 1
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                                                                                                                                                                         Perfect score:
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28432 110 112 112 113 113

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The invention relates to human nucleic acids (AAI57798-AAI61369) and
the encoded polypeptides (AAM38642-AAM42213) with nootropic,
the encoded polypeptides (AAM38642-AAM42213) with nootropic,
limunosuppressant and cytostatic activity. The polynuclectides are useful
in gene therapy. A composition containing a polypeptide or polynucleotide
c of the invention may be used to treat diseases of the peripheral nervous
system, such as peripheral nervous injuries, peripheral nervous
c system, such as not central nervous system diseases, anch as
localised neuropathies and central nervous system diseases, anch as
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
tulisation of the activities such as: Immune system suppression,
Activin/inhibin activity, chemotactic/chemothetic activity, haemostatic
and thrombolytic activity, cancer diagnosis and therapy, drug screening,
ssays for receptor activity, arthritis and inflammation, leukaemias and
c.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
specification.
                                                                                                                                                                                          Example 2; SEQ ID NO 6504; 10078pp; English.
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279 AA; Sequence

ö Gaps 0 Score 42; DB 22; Length 279; Pred. No. 32; 7; Indels 3; Mismatches 7; Indels Ouery Match
Best Local Similarity 41.2%;
Matches 7; Conservative

49 QGXRXFXXWKGSVVDSV 65

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Search completed: November 8, 2002, 19:25:54 Job time : 16.9706 secs

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In gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and constructions.
                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang D;
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ren F, W
Zhang J;
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                                                                                                                                                                            DB 22; Length 232;
                                                                                                                                                                                                Indels
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Yang Y,
                                                                                                                                                                                                 7;
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 2933; 10078pp; English
                                                                                                                                                                                      Pred. No. 25; ; Mismatches
                                                                                                                                                                             Score 42;
                                                                                                                                                                                                                                                                                                - AAM39788 standard; Protein; 258 AA.
                                                                                                                                                                                                                                                                                                                                                                Human polypeptide SEQ ID NO 2933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0662191.
2000US-0693036.
2000US-0727344.
                                                                                                                                                                            15.3%;
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2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0620312
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                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                      QGXRXFXXWKGSVVDSV 65
                                                                                                                                                                                                                                          34 EGDEPITOWKGTVLDQV 50
                                                                                                                                                                                      Best_Local Similarity 41.2
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                       232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAI58944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2000;
09-JUL-2000;
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29-NOV-2000;
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                                                                                                                                                        Sequence
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                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                          RESULT 14
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, inmunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the Activity the activities such as Immune system 'superssion' Activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, nootropic, immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Zhang J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.3%; Score 42; DB 22; Length 258; 41.2%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qian XB,
Yang Y,
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tu C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM41573 standard; Protein; 279 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 6504.
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Wehrman T, Xu
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-048B725.
2000US-055317.
2000US-059B042.
2000US-065315.
200US-0653150.
200US-0653191.
2000US-0653191.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGDEPITOWKGTVLDQV 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
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Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                      258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAI60729
                                                                                                                                                                                                                                                                                                                     C.N.S disorders.
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19-OCT-2000; 2
29-NOV-2000; 2
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM41573;
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                                                                          Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a cares. The disorders include SAPHO syndrome (synovitis, acne, P. acnes; The disorders include SAPHO syndrome (synovitis, acne, P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgatis. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as the diagnostic agents for determining P. acnes presence, for example, by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enzyme linked immunosorbent assay (ELLSA).
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a polypeptide that is critical for the survival and growth of Candida albicans. The C. albicans nucleic acid molecules encoding the polypeptides of the invention may be used as probes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Candida albicans infection; growth; survival; medicament; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Essential polypeptides isolated from Candida albicans, treatment of diseases caused by C.albicans, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment of diseases caused by C.albicans, especially immunocompromised subjects, e.g., AIDS patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vulvovaginitis; immunocompromised patient; treat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 2
Pred. No. 36;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 WKACLAEGVLCLFLTANDGTMAS----YLAESFP 366
     SEQ ID No 3451; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Candida albicans polypeptide sequence # 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 WKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 59-60; 133pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.6%;
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida albicans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-2000
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     Example 1;
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primers for detecting homologous nucleic acid molecule sequences. The polypeptides and nucleic acid molecules and compounds identified as selectively modulating the expression of the polypeptides, may be used as medicaments or for the preparation of a medicament to treat C.albicans associated diseases, especially in AIDS patients and to treat vulvovaginitis in otherwise healthy females. The use of the polypeptides and polynucleotide sequences to treat C.albicans associated diseases has fewer side effects and less toxicity than previously used methods such as the use of amphotericin. This method is therefore especially suitable for immunocompromised patients, such as AIDS patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang D;
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Haurtington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAMARAA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ren F, W
Zhang J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy;
                                                                                                                                                                                                      DB 21; Length 466; 39;
                                                                                                                                                                                                                                             2; Indels
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Yang Y,
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tu C, Xue AJ,
Drmanac RT;
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                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system injuries
                                                                                                                                                                                                              Score 43;
                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 xu c,
                                                                                                                                                                                                                                                                                                                                                                                       AAM39787 standard; Protein; 232 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 2932.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asundi V, C/
                                                                                                                                                                                                            15.6%;
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2000US-0653450
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2000US-0693036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-2001 (first entry)
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             such as central nervous
                                                                                                                                                                                                                                                                           57 WKGSVVDSVXGV 68
                                                                                                                                                                                                                                                                                                          79 WEGSVLDPIEGI 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-442253/47.
                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                             466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C,
Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAI58943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2000;
19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JAN-2000;
                                                                                                                                                                                                                                            ;9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                      AAM39787;
                                                                                                                                                                               Sequence
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                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel
                                                                                                                                                                                                                                                                                                                                                        RESULT 13
AAM39787
                                                                                                                                                                                                                                            Matches
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related polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU42256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
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                                                                                                                                                             The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA019300) that exhibit activity elating to cytokine. cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity in activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                 treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buchrleser C, Frangeul L, Couve E, Rusniok C, Faihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P, Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                      Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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                                                                                                                              Claim 20; SEQ ID NO 18456; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 22; Length 106;
Pred. No. 4.2;
2; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listeria monocytogenes protein #991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB48287 standard; Protein; 434 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 MXXXQGXRXFXXWKGSVVDSVXGVFL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 MLGVQGASRFGVWGGAVSWSIDGAVL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.0%;
ilarity 38.5%;
Conservative 2
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WPI; 2001-514838/56.
N-PSDB; AAI84495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200177335-A2.
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The present invention relates to the genome sequence of Listeria

monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
it are useful for selecting probes and primers for detecting genes in L.

monocytogenes and related organisms, and for studying genetic
color polymorphisms and other genomes. The present sequence is a protein
cerocade by the genome sequence of the present invention. Proteins
expressed from the genome sequence are useful for raising specific
antibodies, identification of L. monocytogenes and related organisms, and
for lossynthesis and blodegradation, especially blossynthesis of Vitamin
B12. The genome sequence and proteins encoded by it are also useful for
selecting compounds that regulate gene expression and cell replication
and modulate L. monocytogenes related diseases. In addition, the genome
sequence and proteins encoded by it are useful in pharmaceutical and
vaccines compositions for the treatment or prevention of infections by L.
monocytogenes and related organisms.
CC Note: The sequence data for this patent did not form the printed
specification, but was obtained in electronic format directly from WIPO
cx t ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalnitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 23; Length 434;
Pred. No. 36;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes immunogenic protein #3152.
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L'maisonneuve J, Zhang Y, Jen S, Carter D;
Claim 6; SEQ ID No 992; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU42256 standard; Protein; 436 AA
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 57.1 nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 VDSVXGVFLTQNXD 75
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WPI; 2001-318749/34
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                                                                                                                                                                               the treatment, proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO Syndrome (synovitis, acne, practices and osteomycelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lessions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a ample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes properly by P. acnes protein in the sample, by acnes infections. The antibodies may also be used as clargment inked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed a per interval in the sample, by the feature of the printed and th
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                                                                                                                                                                     AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.5%; Score 48; DB 22; Length 235; 32.0%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                   Example 1; SEQ ID No 7822; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein sequence SEQ ID NO:12081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB93159 standard; Protein; 882 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 QGXRXFXXWKGSVVDSVXGVFLTQN 73
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                    treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HELI-) HELIX RES INST.
               WPI: 2001-616774/71
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                                 N-PSDB; AAS59534,
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Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB93159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence 1s selected from those defined in the specification: The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13678 and AAH18633 to AAH18672 represent human cDNA sequences; AAB9446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vacchie; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 882;
24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Indels
                                                                                                                                                                                     Claim 8; SEQ ID 12081; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.7%; Score 46; 33.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 RXFXXWKGSVVDSVXGVFLTQNXDXXS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       882 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Disclosure; Page 75; 109pp; English.

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complement encoding a polypeptide having a sequence at least 40%

identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B

or Cor their combinations. Also included are an expression

cassette comprising the polynuclectide or comprising a heterologous

DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated

comparison of DMT, a host cell comprising an exogenous polynucleotide

concing a DMT-like protein. The expression cassette is

concing a DMT-like protein. The expression cassette is

concing a DMT-like protein. The expression cassette is

concing a DMT-like protein. The method comprises introducing

the cassette into a host cell preferably Agrobacterium by sexual

consolidation is capable of exhibiting at least one of the following

concing a protein is capable of exhibiting at least one of the following

biological activities, which include enhanced expression of the

protein in a plant results in a delay in flowering time, introduction of

chromosomal DNA in the cell, reduction of expression of the protein in a

plant results in enhanced endosperm development and expression of the

chromosomal DNA in the cell, reduction of expression of the protein in a

plant results in enhanced endosperm development and expressing of the

chromosomal DNA in the cell, reduction of expression of the Protein in a plant results in expression of the protein in a contract of the protein in a sample.

Concording the contract of the protein and expression of the protein of the protein in a plant results of the protein in a plant present for detecting a nucleic acid in a sample.

Concording the contract of the present 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23; Length 1952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Demeter; DMT: Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation: transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hannon M, Okamuro JK, Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 162.5; DB 23; Length
Pred. No. 2.7e-20;
); Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          926 RFSPWKGSVVDSVVGVFLTQNVSDHLSSSAFMALAAKFP 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU72741 standard; Protein; 1114 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis DMT4 (1DMT4) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis Thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1952 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Bëst Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS96694.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
          δ
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                                                                                                                                                                                                    bolynucleotide encoding a by Tilke protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of the protein in an Arabidopsis leaf results in expression of the MEDEA gene protein in an Arabidopsis leaf results in expression of the MEDEA gene protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylation. The present transcription of target genes by demethylation. The present
                              The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETRE, previously known as ATROPOS (ATR)) Domain A, Bo or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             403 KVNLDPETIKEWDVLMVNDSPSRSYDDKETEAKWKKEREIFQTRIDLFINRMHRLQGNRK 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KVXXDXXTXXXWXXL-----XXXXDXXXXXXXXXXXERXXEXXXEXXXXXIXRXXXQGXRX 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 162; DB 23;
Pred. No. 1.7e-20;
0; Mismatches 47;
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Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 FXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents a DMT-like protein.
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, Jen S, Ca
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2000US-208841P.
2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L'maisonneuve J,
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02-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
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AAU46627
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region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a encoding a DMT-like protein and a transgenic plant comprising a polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of their protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. The polynucleotide to S-methylstytosine glycosylases and regulates transcription of target genes by demethylation. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising a sequence or C -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DWT (DEMETER, previously known as ATROPOS (ATR)) Domain A, or C or their combinations. Also included are an expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 697 KVDIDDETTRIWNLIMGKGDEKEGDEEKDKKKEKWWEEERRVFRGRADSFIARMHLVQGD 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KVXXDXXTXXXXXXXXXXXXXXXXXXXXXXXXXXXXERXXFXXXXXXIXRMXXXQGX 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                       Length 1729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide that control plant development having a specific homology to DEMETER domains A,B
                                                                                                                                                                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                                                                                                                                         DB 23;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 59.6%; Score 164; DB 23; Best Local Similarity 43.0%; Pred. No. 1.3e-20; Matches 43; Conservative 0; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 67; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU72737 standard; Protein; 1413 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis DMT2 (1DMT2) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-2001; 2001WO-US13059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis Thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                 1729 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS96692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200180626-A1.
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                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                  polynucleotide encoding a by Talke protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the call, reduction of expression of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylation, The present transcription of target genes by demethylation. The present
cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KVXXDXXTXXXWXXL-----XXXXDXXXXXXXXXXXERXXFXXRXXXXFIXRMXXXQGXR 52
                                                                                                                                                                                                                                                                                                                                                                                                          Score 163.5; DB 23; Length 1413;
Pred. No. 1.2e-20;
0; Mismatches 47; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
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                                                                                                                                                                                                                                                                                                                                        sequence represents a DMT-like protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU72743 standard; Protein; 1952 AA
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 43.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-055307/07.
                                                                                                                                                                                                                                                                                                                                                                           Sequence 1413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice DMT1 protein.
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AAU72743
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26-FEB-2002
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                              The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
                                                                                                                                                                                                                                                                                                                                 497 KVQLDPETSRVWKLLMSSIDCDGVDGSDEEKRKWWEEERNMFHGRANSFIARMRVVQGNR 556
                                                                                                                                                                                                                                                                                                  DB 23; Length 1309;
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DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
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SEQ ID NO 1471; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                3.1e-21;
Thes 47;
                                                                                                                                                                                                                                                                                                                                                                                  53 XFXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
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Pred. No. 3.1e-
0; Mismatches
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                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fischer RL, Choi Y,
                                                                                                                                                                   useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis Thaliana
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                                                                                                                                                                                                   1309 AA;
                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                   Sequence
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 Claim 5;
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Matches
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                                                                                                                                                                       protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in a plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylcytosine glycosylases and regulates transcription of target genes by demethylation. The present sequence represents a DMT-like protein.
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useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497 KVQLDPETSRVWKLLMSSIDCDGVDGSDEEKRKWWEEERNMFHGRANSFIARMRVVQGNR 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KVXXDXXTXXXWXXLXXXXDXXXXXXXXXXXXXXXXEXXFXXXXXFIXRMXXXQGXR 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1332;
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DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.5%;
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8, 2002, 19:24:08; Search time 13.9706 Seconds (without alignments) 858.415 Million cell updates/sec
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1 KVXXDXXTXXXWXXLXXXXD.....TQNXDXXSSXAXMXXAXXFP 90
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS2/gcgdata/geneseqg-emb1/AA1985.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT;
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT;
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/SIDS2/gcgdata/geneseg/genesegp-embl/AA1999.DAT.
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908470
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                            US-09-840-743-71
                                                                                                                                                                                       November
                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Herbicidally activ	Arabidopsis DMT3	Arabidopsis Deme	Arabidopsis DMT2	Rice DMT1 protein	Arabidopsis DMT4	Propionibacteriu	Human protein se	Human polypeptide	Tictoria monoria
	ID	ABB92260	AAU72739	AAU72736	AAU72737	AAU72743	AAU72741	AAU46627	AAB93159	AAO04564	ABB48287
	DB	23	23	23	23	23	23	22	22	22	23
	Query Match Length DB ID	1309	1332	1729	1413	1952	1114	235	882	106	131
ar (	Query	60.5	60.5	59.6	59.5	59.1	58.9	17.5	16.7	16.0	4
	Score	166.5	166.5	164	163.5	162.5	162	48	46	44	٧ ٦
	No.	-	7	٣	4	5	9	7	80	6	10

11	43	15.6	436	22	AAU42256	ibacterium
12		15.6	466	21	AAY95051	Ö
13	42	15.3	232	22	78	Human polypeptide
14	42	15.3	258	22	T)	Human polypeptide
15	42	15.3	279	22	AAM41573	Human polypeptide
16	42		279	22	AAM41574	Human polypeptide
17	42	15.3	370	22	AAB93450	Human protein segu
18	42		370	23	AAB47993	
19	42		973	19	AAW48304	Amino acid sequenc
20	41.5	S.	351	22	AAU50778	0
21	41	4.	331	22	ABG10353	human
22	41	•	453	22	ABG12472	human
23	41	4	973	23	ABB97191	human
24	4	•	973	23	ABB05701	Human intracellula
25	•	14.7	84	20	AAY11870	
26	40.5	14.7	310	23	ABB92345	
27	40	•	159	23	ABP38906	Ξ
28	40	4	196	23	ABP30378	_
53	40	٠	200	23	ABP28344	coccus
30	40	4	211	21	AAY51682	clodin
31	40	4	313	21	AAY90872	Human G protein-co
32	40	4.	313	22	AAU10306	tei
33	40	14.5	313	22	AAG72077	olfactor
34		4	318	20	AAW90108	FLAME-2
32		4	318	20	AAW90109	FLAME-2
36	40	4	318	21	AAY51022	DEDD
37		4	318	21	AAY51023	(I)
38		4.	318	22	AAB93016	prote
39	40	4.	318	22	AAB94040	Human protein sequ
40	40	4	1140	22	AAE09365	Human ATP-binding
41	40	4.	18	22	AAM93387	Human polypeptide,
42	40	4.	1503	20	AAY43544	A human MPR-relate
43.	40	4.	50	22	AAE09361	Human ATP-binding
44	40	4	1503	22	AAE09363	Human ATP-binding
	40	4	20	22	AAE09364 .	Human ATP-binding
					ALIGNMENTS	
ESULT 1						
BB92260 D ABR92260		standard:	Profein		1309 AA	
×				i		
C ABB92260	2260;					
	31-WAY-2002		(first ontru)	:		

Herbicidally active polypeptide SEQ ID NO 1471. Herbicidal; plant; agriculture; herbicide. 28-AUG-2001; 2001WO-EP09892. 28-AUG-2001; 2001WO-EP09892 31-MAY-2002 (first entry) Weidler M; Arabidopsis thaliana. (FARB ) BAYER AG. WO200210210-A2. 07-FEB-2002 Tietjen K, 

Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms

WPI; 2002-269010/31.

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610-407-0700
                                                                                                                                                                50 GXRXFXXWKGSV 61
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                                                                                                                                                                                                                                                                                                                                                                                       13.8%; Score 38; DB 4; Length 634; 58.3%; Pred. No. 1.6e+02; ative 0; Mismatches 5; Indels
                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
SUBTRANT DATE: March 11, 1998
CLASIFICATION NUMBER: US/09/041,236
FILING DATE: March 11, 1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: SEL98-001
FELEPHONE: (650) 343-434
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 634 amino acids
TYPE: AUTORNAME OCID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 23,031
REFERENCE/ZDOCKET NUMBER: GP-30039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                        Query Match 13.8
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-041-236-2
HILLSBOROUGH
                                                                                                                                                                                                                                                                                                                                                                  CALIFORNIA
: USA
                                                                                                                                                                                                                                                                                                                                                    50 GXRXFXXWKGSV 61
                    COUNTRY:
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| TELEX. | 10.0.40 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.00 | 10.0.
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Sequence 2, Application US/09041236
Fatent No. 6225285
GENERAL INFORMATION:
APPLICANT: Luo, Yuling
APPLICANT: Alomei, Xan
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 2;
Pred. No. 37;
3; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 EXECUTIVE SQUARE, STE 1400
CITY: LA JOLLA
CTATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,359A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09010/010001
                                                                                                      Sequence 33, Application US/08602359A Patent No. 5942430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       February 16, 1996
                                                                                                                                                                                                                               APPLICANT: MAFFIA, Anthony
APPLICANT: LINK, Steven
APPLICANT: SWANSON, RODALD V.
APPLICANT: WARREN, PATRICK V.
APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 GXRXFXXW---KGSVVDSVXGVFL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFRENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 GLRNLYSWSRVKGSLIISM-GVFL 94
                                                                                                                                                GENERAL INFORMATION:
APPLICANT: ROBERTSON, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619-678-5099 INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                          MURPHY, Dennis
REID, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 184 AMINO ACIDS
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 13.8 Best Local Similarity 45.8 Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: PROTEIN US-08-602-359A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92037
                                                               RESULT 13
US-08-602-359A-33
                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-041-236-2
                                                                                                                                 ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Steven P. Fling
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: COMPOSITIONS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 317
                              APPLICANT: Dalrymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 491;
78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 14.2%; Score 39; DB 4; Length 646; Best Local Similarity 27.0%; Pred. No. 1.1e+02; Matches 10; Conservative 4; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
AURIZATION NUMBER: US/08/206,176
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 RXXXFIXRMXXXQGXRXFXXWKGSVVDSVXGVFLTQN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 317, Application US/09620412C
patent No. 6448234
                                                                                                                                                                                          E: ZymoGenetics, Inc.
4225 Roosevelt Way, N.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.28;
47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 WKGDKVKAHYGGFTVON 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 14.2
Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 WKGSVVDSVXGVFLTQN 73
                     Garner, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-206-176-4
GENERAL INFORMATION:
                                                                                                                                                                                          ADDAL.
STREET: 422.
"TW: Seattle
                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                STATE: WA
COUNTRY: USI
ZIP: 98105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-620-412C-317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-620-412C-317
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326 RTLAFINNMSGDCGGAISADTQISITDTVKGILFENN 362
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Gaps
             4
Length 184;
            Indels
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MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-206-176-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-213-053-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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Sequence 6, Application US/09276993

Patent No. 6207801

GENERAL INFORMATION:
APPLICANT: Alloemri, Emad S.
APPLICANT: Alloemri, Emad S.
APPLICANT: Fernandez-Alnomri, Teresa
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS TITLE OF INVENTION: Of MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801ris
STREET: One Liberty Place, 46th floor
                                                                                                APPLICANT: Alnemit, Emad S.
APPLICANT: Fernandez-Alnemit, Teresa
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: OF MAKING THE SAME
COMPOSITIONS FOR AND METHODS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                    ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.5%; Score 40; DB 4; Length 318; 33.3%; Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: WINDOWS .
SOFTWARE: Wordberfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
                                      Sequence 4, Application US/09276993
Patent No. 6207801
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 229
REFERENCE/DOCKET NUMBER: 7JI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 WRDYINGSLLEALKGVFITDS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 WK----GSVVDSVXGVFLTQN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.5
Best Local Similarity 33.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-09-276-993-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                          PA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                   STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-276-993-6
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GENERAL INFOGRATION:
APPLICANT: AUDONNET, Jean-Christophe
APPLICANT: AUDONNET, Jean-Christophe
APPLICANT: AUDONNET, Jean-Christophe
TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
FILE REFERENCE: 454313-2200
CURRENT APPLICATION NUMBER: 9608242
EARLIER APPLICATION NUMBER: 9608242
EARLIER APPLICATION NUMBER: PCT/FR97/01115
EARLIER PILING DATE: 1996-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENT VEIL VEIL 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 4
Pred. No. 31;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.2%; Score 39; DB 36.8%; Pred. No. 61; Live 4; Mismatches
                           COMPUTER: IBM PC COMPALLLL
COMPUTER: WINDOWS
SOFTWARE: WORDFERT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,993
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
APPLICATION NUMBER: 08/859,167
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA, MARK
REGISTRATION NUMBER: TJU-
TELECHOME: (215) 568-3100
TELECHOME: (215) 568-3439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids

"NINDER SECOND SECO
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; Patent No. 5639940
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Patent No. 6159477
: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 WK----GSVVDSVXGVFLTQN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 14.5%;
Best Local Similarity 33.3%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 RXFXXWKGSVVDSVXGVFL 70
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Best Local Similarity 36.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-09-276-993-6
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Gaps

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GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Alnemri, Emad S.

APPLICANT: Alnemri, Emad S.

APPLICANT: Alnemri, FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS TITLE OF INVENTION: Of MAKING THE SAME, AND COMPOSITIONS FOR AND METHODS TITLE OF INVENTION: 0. MAKING THE SAME
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760ris STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                         Score 40; DB 3; Length 318;
Pred. No. 31;
8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ced. No. 31;
Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-109-273-6; Sequence 6, Application US/09109273; Patent No. 6063760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: DeLuca, Mark
REGISTRATION UNDHER: 33,229
REPERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEFONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                    œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                    260 WRDYINGSLLEALKGVFITDS 280
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                                                                                                                                                                                                           14.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 WK----GSVVDSVXGVFLTQN 73
                 TELEFAX: (215) 568-9439
FINFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: protein
US-09-109-273-4
  (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.5%;
                                                                                                                                                                                      Query Match
Best Local Similarity 33.35,
Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-09-109-273-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
7, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
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APPLICANT: Fernandez-Alnemit, Teresa
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: Of MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.5%; Score 40; DB 3; Length 318; 33.3%; Pred. No. 31; Live 8; Mismatches 2; Indels
: One Liberty Place, 46th floor Philadelphia
                                                                                                                                                                               SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/109,273 FILING DATE:
                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA: MATK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR ESO ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: WORDPEFECT
CURRENT APPLICATION DATA:
                                                         COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09109273
Patent No. 6063760
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 WRDYINGSLLEALKGVFITDS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: DeLuca, Mark
RECISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 WK----GSVVDSVXGVFLTQN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.5
Best Local Similarity 33.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-859-167-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Phil
STATE: PA
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US-09-109-273-4
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Gaps

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Length 318; Indels

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GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Alnemri, Teresa
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: OF MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
TITLE OF INVENTION: Of MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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      DB 4; Length 159;
                                                                23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                 DB 3;
                                                                                                                             54 FXXWKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
                                                                5; Mismatches
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   14.5%; Score 40; 24.3%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08859167
Patent No. 6037461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33, 229
REFERENCE/DOCKET NUMBER: TUU-
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08859167
Patent No. 6037461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 WRDYINGSLLEALKGVFITDS 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Alnemri, Emad S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 33.3.
The Conservative 
                                                                   9; Conservative
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   Query Match
Best Local Similarity
Matches 9; Conserv
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STATE: PA
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US-08-859-167-4
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Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE OF INVENTION UNMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3751
LENGTH: 159
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                                                                                                                                                                                                                                                                                              CITY: Emeryville
STATE: California
COUTRY: 0.S.A.
2IP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,639
                Sequence 4, Application US/09517639
Patent No. 6414120
GENERAL INFORMATION:
APPLICANT: Randazzo, Filippo M.
APPLICANT: Randazzo, Filippo M.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
51;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/904,452
FILING DATE: 31-JUL-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                           ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Potter, Jane E.R. REGIESTRATION NUMBER: 33,332 REFERENCE/DOCKET NUMBER: 12. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (510) 923-2718
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Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
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US-09-517-639-4
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ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461ris

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Best Local Similarity 47.1
Matches 8; Conservative
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                                                                                                                                                               .; Search time 5.14706 Seconds (without alignments) 514.481 Million cell updates/sec
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275
1 KVXXDXXTXXXWXXLXXXXD.....TQNXDXXSSXAXMXXAXXFP
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-517-639-4
US-08-859-167-4
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US-09-109-273-4
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US-09-273-6
US-09-276-993-6
US-09-276-993-6
US-09-276-993-6
US-09-2412-317
US-09-627-412-317
US-09-627-412-3
US-09-199-637A-405
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US-08-471-119A-2
US-08-858-207A-363
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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US - 08 - 6 US - 08 - 6 US - 09 - 3 US -	ALIGN ALIGN M. Deep   10,452 04,452	Score Pred. 1
	4 1 d 4 e e e e e e e e e e e e e e e e e e	2
ここよねよなことなるようことなるように	/08904 	15.3%; 47.1%; ive
1213 1443 14443 14443 1467 22115 22133 22133 3898 3898 3898 365 900 108	1-4 Application US/08904452 6083742 FUCRMATION: TH: Randazzo, Filippo M. TH: Randazzo, Filippo M. THENENTION: Mammalian D F SEQUENCES: 4 4560 Horton Corporation Emeryville California California THENENTY INS. 94668-2916 THENEYVILLE TORNEY THENEYVILLE TORNEY THENEYVILLE TORNEY THENEYVILLE TATION THENEY T	15. Larity 47. Conservative
	Phication U MATION: MATION: MATION: MENTION: M EQUENCES: MCE PADRESS: MCE Chiron C 456 Horton C 456 Horton 456 Horton 456 Horton 457 Horton 108 -234. MARABLE FORM PE: FLORM PE: FLORM PE: FLORM NUMBER: MATION: 435 ATION NUMBER: MATION NUMBER: MATI	ity
	-4 Application 6083742 T: Randazzo INVENTION: FSEUGNCES: NDENCES: NDENCES: NDENCES: TY: 4560 HOTE EMETYILE California Tr. 0.5.A. 94608-2916 READABLE FO TYPE: FLOP ER: Datenti APPLICATION: 4 APPLICATION A ATION NUMBER DATE: 31-J FLOATION TOWNER DATE: 31-J FLOATION TOWNER ONE: (510) ONE: (510) CHARACTERIS: N FOR SEO ID CHARACTERIS N FOR	Similarity 8; Conser
32 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	ULT 1  08-904-452-4  equence 4, Application US/08904  atent No. 6083742  GENERAL INFORMATION:  APPLICANT: Randazzo, Filippo TITLE OF INVENTION: Mammalia NUMBER OF SEQUENCES: 4  CORRESPONDENCE ADDRESS: 4  CORRESPONDENCE ADDRESS: 4  COUNTRY: U.S.A.  ZIP: 94600-2916  COMPUTER READABLE FORM: MEDIUM TYPE: FLORPY disk  COMPUTER: BM PC Compatibl  OPERATING SYSTEM: PC-DOS/M  SOFTWARE: BACHELL Release  CURRENT APPLICATION DATA: 33-33  REGISTRATION NUMBER: US/08/ FILING DATE: 31-JUL-1997  CLASSIFICATION NUMBER: 33-33  REFERENCE/DOCKET NUMBER: 33  REFERENCE/COCKET NUMBER: 31-31  TELECOMMUNICATION INFORMATION  TELEPHONE: (510) 655-3542  INFORMATION FOR SEQ ID NO: 4:  SEQUENCE CHARACTERISTICS:  LENGTH: 973 amino acids  STRANDEDNESS: single  TOPOLOGY: linear  MOLECULE TYPE: protein	
	SULT 1 Sequence 4, A SULTILE OF I NUMBER OF CORRESPOND ADDRESSE STRATE: CITY: CITY: COUNTRY: COUNTRY: COUNTRY: COUNTRY: COUNTRY: COUNTRY: COUNTRY: COUNTRY: COUNTRY: CITY: COUNTRY: CITY: COUNTRY: CITY: COUNTRY: CITY: COUNTRY: CITY: CITY: COUNTRY: CITY: CI	y Match Local hes
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Search completed: November
Job time: 4.79412 secs
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                                                                       TYPE: PRT
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                                                                                                                                                                                                          APPLICANT: FLECKENSTEIN, Bernhard
APPLICANT: FLECKENSTEIN, BERNHARD
ENSSER, Armin
TITLE OF INVENTION: HUMAN SEMAPHORIN L (H-SEMAL) AND
CORRESPONDING SEMAPHORINS IN OTHER SPECIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Frommer Lawrence & Haug LLP
STREET: 745 Fifth Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lawrence, William F.
REGISTRATION NUMBER: 28,029
REFERENCE/DOCKET NUMBER: 514429-3647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INCORMATION:
APPLICANT: David Michalovich
APPLICANT: David Michalovich
APPLICANT: Philip David Hayes
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30039-D1
CURRENT APPLICATION NUMBER: US/09/764,587A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 09/240,410
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/836,077
FILING DATE: 16-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: amino acid
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-836-077-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEFAX: 212-588-0500
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09764587A Patent No. US20020106722A1
                                                                                                                                                    Sequence 3, Application US/09836077 Patent No. US20020037851A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 666 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                        86 GIFTTPNFDETSSATTISTS 105
67 GVFLTQNXDXXSSXAXMXXA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: n/a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Matches 7; Conserva
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                                                                                                           RESULT 13
US-09-836-077-3
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APPLICANT: Williamson, Mark
TITLE OF INVENTION: No. US20020034780Alel Human Protein Kinases and Uses
TITLE OF INVENTION: Therefor
FILE REFERENCE: 35800/20996
CURRENT APPLICATION NUMBER: US/09/799,875
CURRENT APPLICATION NUMBER: 06/182,059
PRIOR APPLICATION NUMBER: 60/182,059
PRIOR APPLICATION NUMBER: 09/659,287
PRIOR FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Fast5EQ for Windows Version 4.0
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                                                                                                                                                            Length 666;
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                                                                                                                                                                                              Indels
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                                                                                                                                                          DB 10;
53;
                                                                                                                                                        Score 38; DB 1
Pred. No. 53;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 KGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 666
                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/09799875 ; Patent No. US20020034780A1
                                                                                                                                                        13.8%;
ilarity 58.3%;
Conservative (
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                                                                                               ; ORGANISM: HOMO SAPIENS
US-09-764-587A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-799-875-2
                                                                                                                                                                                                                                  50 GXRXFXXWKGSV 61
                                                                                                                                                                                                                                                                   51 GPRIFAVWKGHV 62
                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
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Xaa equals any of the naturally occurring L-amino acids
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SPETMARE: PatentIn Ver. 2.0
SEQ ID NO 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xaa equals any of the naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 210;
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Pred. No. 14;
5; Mismatches 26; Indels
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                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFFWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 GPAIFIGWAGSALVILGGALLSCSCPGNESKAGYRAPRSYP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 GXRXFXXWKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
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                                                                                                APPLICATION NUMBER: US/09/935,390A
FILING DATE: 22-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                             NAMÉ: Jane E. R. Potter
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 1369.002
TELECOMMUNICATION ITELEPRATION:
TELEPHONE: (510) 923-218
TELEPAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: No. US20020076761Ale SEQUENCE DESCRIPTION: SEQ ID NO: 36.05-09-935-390A-36
                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/988,671
FILING DATE: 1997-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-764-864-1235
; Sequence 1235, Application US/09764864
; Patent No. US20020132753A1
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 210 amino acids
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
  MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.8%;
24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                       TELEX: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 10; Conserv
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; OTHER INFORMATION:
US-09-764-864-1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (14)
OTHER INFORMATION:
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LOCATION: (488)
OTHER INFORMATION:
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TITLE OF INVENTION: ENZYMES HAVING ESTERASE ACTIVITY AND METHODS OF USE THEREOF
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                                                                                                    DB 10; Length 646;
                                                                                                                                           Indels
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Milliams, Lewis T.
Kothakota, Srinivas
TITLE OF INVENTION: Secreted Human Proteins
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 10;
Pred. No. 12;
                                                                                                                                                                                                           326 RTLAFINNMSGDCGGAISADTQISITDTVKGILFENN 362
                                                                                                                                                                                 37 RXXXFIXRMXXXQGXRXFXXWKGSVVDSVXGVFLTQN 73
                                                                                                                          Pred. No. 34;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
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CURRENT APPLICATION NUMBER: US/09/903,410
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/382,242
PRIOR APPLICATION NUMBER: US 08/602,359
PRIOR PRIOR PLING DATE: 1999-08-24
PRIOR PRICATION NUMBER: US 08/602,359
PRIOR FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
                                                                                                  Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36, Application US/09935390A Patent No. US20020076761A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            Sequence 33, Application US/09903410 Patent No. US20020146799A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Staphylothermus Marinus US-09-903-410-33
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                     ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-841-132-317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Escobedo, Jaime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.8%;
Best Local Similarity 45.8%;
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DIVERSA CORPORATION
                                                                                                  Query Match
Best Local Similarity 27.0%;
Matches 10; Conservative
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ZIP: 94608-2916
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAFFIA, Anthony
LINK, Steven
SWANSON, Ronald
WARREN, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Emeryville STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                          ROBERTSON, Dan
MURPHY, Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REID, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-09-935-390A-36
                                                                                                                                                                                                                                                                                                     US-09-903-410-33
LENGTH: 646
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APPLICANT:
APPLICANT:
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APPLICANT: Colliner, Alan
APPLICANT: Alfano, James R.
APPLICANT: Alfano, James R.
APPLICANT: Alfano, James R.
APPLICANT: Charkowski, Amy O.
TITLE OF INVENTION: HRP PATHOGEULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE
TITLE OF INVENTION: HRP PATHOGEULEY ISLAND AND THEIR USES
FILE REFERENCE: 19603/3243
CURRENT APPLICATION NUMBER: 05/09/825,414
CURRENT FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 91
SOFTWARR: PATENTIN VOET: 2.1
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APPLICANT: Bhatia, Ajay
APPLICANT: Bhatia, Ajay
APPLICANT: SESIKY, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND FILE REFERENCE: 210.121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastESQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                            DB 10; Length 305;
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.2%; Score 39; DB 10; Length 316; 53.8%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Pseudomonas syringae pv. delphinii
US-09-825-414-56
                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                 Score 39;
Pred. No.
PRIOR APPLICATION NUMBER: 60/178,227
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/220,590
PRIOR FILING DATE: 2000-07-25
NUMBER OF SEO ID NOS: 95
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 317, Application US/09841132 Patent No. US20020061848A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-825-414-56
; Sequence 56, Application US/09825414
; Patent No. US20020083489A1
                                                                                                                                                                                                                                                                                                 14.2%;
38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                        54 FXXWKGSVVDSVXGVFLT 71
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 38.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 53.8
Matches 7; Conservative
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                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-761-288-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 KGSVVDSVXGVFL 70
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US-09-841-132-317
                                                                                                                                                                        LENGTH: 305
                                                                                                                                                                                               TYPE: PRT
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APPLICANT: Padigaru, Muralidhara
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Taupier, Raymond J
APPLICANT: Taupier, Vishuu
APPLICANT: Tolernew, Velizar
APPLICANT: Tolernew, Velizar
APPLICANT: Tolernew, Velizar
APPLICANT: Li, Li
TITLE OF INVENTION: No. US20020065405Alel Polypeptides and Nucleic Acids Encoding Sam
FILE REFRENCE: 15966-638
CURRENT APPLICATION NUMBER: US/09/761,288
FILE REFRENCE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/176,334
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/216,389
PRIOR FILING DATE: 2000-07-14
PRIOR PRIUCATION NUMBER: 60/220,253
PRIOR APPLICATION NUMBER: 60/220,253
PRIOR FILING DATE: 2000-07-24
                                                                                                                                                                                                                                                                                                                             APPLICANT: COllmer, Alan
APPLICANT: Collmer, Alan
APPLICANT: Collmer, Alan
APPLICANT: Alfano, James R.
APPLICANT: Alfano, James R.
APPLICANT: Charkowski, Amy O.
ATTLE OF INVENTION: DNA MOLECULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE
TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
CURRENT APPLICATION NUMBER: 05/194,160
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/224,604
PRIOR FILING DATE: 2000-08-11
PRIOR PRIOR APPLICATION NUMBER: 60/249,548
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 22
LENGTH: 241
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     Length 164;
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                                                  Indels
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  DB 10;
                                                  10;
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Pred. No. 11;
2; Mismatches 4
14.4%; Score 39.5; D
ilarity 37.0%; Pred. No. 5.7;
Conservative 4; Mismatches
                                                                                                                           126 KGEVADLTISLAGKIISQNLDSHAHKA 152
                                                                                             58 KGSVVD---SVXGVFLTQNXDXXSSXA 81
                                                                                                                                                                                                                                                                Sequence 22, Application US/09825414 Patent No. US20020083489A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 86, Application US/09761288 Patent No. US20020065405A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT; ORGANISM: Pseudomonas syringae
US-09-825-414-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.2
Best Local Similarity 53.8
Matches 7; Conservative
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66 KGQLIDLVSGAFL 78
Query Match
Best Local Similarity
Matches 10; Conservat
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US-09_761-288-86
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APPLICANI: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: 05/99/815,242

CURRENT APPLICATION NUMBER: 06/19,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-110-23

PRIOR FILING DATE: 2000-110-22

PRIOR FILING DATE: 2000-110-22

PRIOR FILING DATE: 2000-110-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-20-16
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Pred. No. 5.7;
                       CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR DATE: 2000-05-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARR: FastesD NOS: 14110
SEQ ID NO 13509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13630
            CURRENT APPLICATION NUMBER: US/09/815,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13630, Application US/09815242 Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 KGSVVD---SVXGVFLTQNXDXXSSXA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Streptococcus pneumoniae US-09-815-242-13509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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37.08;
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
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US-09-815-242-13630
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TITLE OF INVENTION: Protein for Regulation of Apoptosis
CURRENT APPLICATION NUMBER: US/09/733,167
CURRENT APPLICATION NUMBER: US/09/733,167
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: PCT/DE99/01712
PRIOR PELING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: German Patent Application No. US20020099009A1 198 25 621.3
PRIOR FILING DATE: 1998-06-08
NUMBER OF EGO ID NOS: 8
SOFTWARE: Patentin Version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/733,167
CURRENT APPLICATION NUMBER: US/09/733,167
CURRENT APPLICATION NUMBER: US/05-12-08
PRIOR APPLICATION NUMBER: GCT/DE99/01712
PRIOR FILING DATE: 1999-06-08
PRIOR FILING DATE: 1998-06-08
NUMBER OF SEC ID NOS: 8
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
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Pred. No. 9.9;
8; Mismatches 2; Indels
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09733167
Patent No. US20020099009A1
GENERAL INFORMATION:
APPLICANT: Peter, Marcus
APPLICANT: Krammer, Peter
TITLE OF INVENTION: Protein for Regulation of Apoptosis
FILE REFERENCE: 4121-120
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 WRDYINGSLLEALKGVFITDS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 WK----GSVVDSVXGVFLTQN 73
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 33.3%;
Matches 7; Conservative 8
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                                                                                                                                                                                                                                                                             LENGTH: 318
TYPE: PRT
CRGANISM: Homo sapiens
US-09-733-167-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-733-167-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 7; Conserv
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
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Gaps

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OM protein - protein search, using sw model Run on:

8, 2002, 19:26:04; Search time 2.79412 Seconds (without alignments) 464.428 Million cell updates/sec . November

Title: Perfect score:

US-09-840-743-71 275 1 KVXXDXXTXXXWXXLXXXXD.....TQNXDXXSSXAXMXXAXXFP 90 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

92612 Total number of hits satisfying chosen parameters:

92612 segs, 14418503 residues

Searched:

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published\_Applications\_AA:\*

1: \cgn2\_6/ptodata/1/pubpaa/USO8\_NEW\_PUB.pep:\*

2: \cgn2\_6/ptodata/1/pubpaa/USO8\_NEW\_PUB.pep:\*

3: \cgn2\_6/ptodata/1/pubpaa/USO6\_NEW\_PUB.pep:\*

4: \cgn2\_6/ptodata/1/pubpaa/USO6\_NEW\_PUB.pep:\*

5: \cgn2\_6/ptodata/1/pubpaa/USO7\_NEW\_PUB.pep:\*

6: \cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\*

7: \cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\*

8: \cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*

9: \cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*

10: \cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*

11: \cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*

11: \cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*

/cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result		% Query				
No.	Score	Match	Match Length DB	DB	OI	Description
1	40	14.5	210	10	US-09-733-167-6	Sequence 6, Appli
8	40	14.5	318	10	US-09-733-167-1	Sequence 1, Appli
რ	40	14.5	318	10	US-09-733-167-3	Sequence 3, Appli
4	39.5	14.4	164	10	US-09-815-242-13509	Sequence 13509, A
Ŋ	39.5	14.4	164	10	US-09-815-242-13630	Sequence 13630, A
9	39	14.2	241	10	US-09-825-414-22	Sequence 22, Appl
7	39	14.2	305	10	US-09-761-288-86	86,
80	39	14.2	316	10	US-09-825-414-56	Sequence 56, Appl
6	39	14.2	646	10	US-09-841-132-317	Sequence 317, App
10	38	13.8	184	10	US-09-903-410-33	Sequence 33, Appl
11	38	13.8	210	10	US-09-935-390A-36	Sequence 36, Appl
12	38	13.8	464	10	US-09-764-864-1235	Sequence 1235, Ap
13	38	13.8	999	10	US-09-836-077-3	Sequence 3, Appli
14	38	13.8	999	10	US-09-764-587A-2	Sequence 2, Appli
15	38	13.8	879	10	US-09-799-875-2	Sequence 2, Appli
16	37.5	13.6	167	10	US-09-815-242-13543	Sequence 13543, A
17	37.5	13.6	792	10	US-09-995-587A-11	Sequence 11, Appl
18	37	13.5	217	10	US-09-799-777-26	Sequence 26, Appl
19	37	13.5	276	10	US-09-815-242-11729	Seguence 11729, A

Sequence 37331, A Sequence 6, Appli Sequence 42021, A Sequence 11074, A Sequence 11074, A Popular Sequence 216, Apple Sequence 217433, A Sequence 217433, A Sequence 22, Appli Sequence 1702, A Sequence 22, Appli Sequence 170, Apple Sequence 170, A
US-09-864-761-37331 US-10-052-586-6 US-09-864-761-43486 US-09-864-761-42021 US-09-815-242-11074 US-09-912-288-6.055-153 US-09-992-298-723-216 US-09-989-723-216 US-09-989-727-216 US-09-989-727-216 US-09-989-727-216 US-09-989-727-216 US-09-991-073-216 US-09-991-216-216 US-09-991-216-216 US-09-991-216-216 US-09-911-216-216 US-09-911-216-216 US-09-911-216-216 US-09-911-216-216 US-09-911-216-216 US-09-911-216-216 US-09-911-216-216 US-09-911-216-216 US-09-911-216-216
41
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# ALIGNMENTS

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US-09-733-167-6

US-09-733-167-6

Sequence 6, Application US/09733167

Sequence 6, Application US/09733167

Sequence 6, Application US/09733167

Sequence 6, Application US/090908A1

GENERAL INFORMATION:

APPLICANT: Beter, Marcus

APPLICANT: Krammer, Peter

TITLE OF INVENTION: Protein for Regulation of Apoptosis

TITLE OF INVENTION: Protein for Regulation of Apoptosis

TITLE OF INVENTION: Peter

TITLE OF INVENTION: PETER 1200-12-08

CURRENT APPLICATION NUMBER: US/09/733,167

CURRENT APPLICATION NUMBER: US/09/733,167

PRIOR FILING DATE: 1999-06-08

PRIOR FILING DATE: 1999-06-08

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 6

SEX ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: C-DEDD, which is a deletion mutant of human DEDD comprising am CTHER INFORMATION: acids 109-318 of the naturally occurring humna DEDD. US-09-733-167-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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Gaps 4; Score 40; DB 10; Length 210; Pred. No. 6.2; 2; Indels 8; Mismatches 2; Indels 8; Query Match
Best Local Similarity 33.3%;
Matches 7; Conservative 8

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|: |:::::|||::::1152 WRDYINGSLLEALKGVFITDS 172 57 WK----GSVVDSVXGVFLTQN 73 RESULT 2 δλ Op

Sequence 1, Application US/09733167; Patent No. US20020099009A1; GENERAL INFORMATION:
APPLICANT: Peter, Marcus
APPLICANT: Krammer, Peter US-09-733-167-1

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Page

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                                                                                                                                                                                                            Leo C.P., Hsu S.Y., McGee E.A., Salanova M., Hsueh A.J.W.; "DEFT, a novel death effector domain-containing molecule predominantly expressed in testicular germ cells."; Endocrinology 139:4839-4848(1998).
                               Stegh A.H., Schickling O., Ehret A., Scaffidi C., Peterhaensel C., Hofmann T.G., Grumut I., Krammer P.H., Peter M.E.; "DED), a novel death effector domain-containing protein, targeted to the nucleolus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBUNTT: Interacts with caspase-8 and FADD (By similarity).
-:- SUBCELLULAR LOCATION: Cytoplasmic. Translocated to the nucleus during CD95-mediated apoptosis where it is localized in the nucleoli (By similarity).
-:- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.
-:- TISSUE SPECIFICITY: Widely expressed with highest levels in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: Binds strongly and non-specifically to DNA. Induces apoptosis. Inhibits DNA transcription in vitro (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50168; DED; 1.
Apoptrosis; Transcription regulation; Repressor; DNA-binding; Nuclear protein; Alternative splicing.
DOMAIN 25 103 DED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Bone marrow, and Placenta;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                   Pan G.;
"FLDED-1, a novel molecule with a DED-like domain.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                        Thome M., Tschopp J.; "DEDPRO1, a novel DED-containing protein."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao Z., Huang X., Li N., Zhu X., Cao X.;
"A novel gene from human dendritic cell.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      testis.
-!- SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).
                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY TISSUE-Testis; MEDLINE-99049260; PubMed-9832420;
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-98447599; PubMed-9774341;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF083236; AAC33105.1; --
EMBL; AF100341; AAD16414.1; --
EMBL; AF043733; AAC80280.1; --
EMBL; AJ010973; CAA09445.1; --
EMBL; AF064605; AAC17110.3; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC016724; AAH16724.1;
EMBL; BC013910; AAH13910.1;
Genew; HGNC:2755; DEDD.
                                                                                                               EMBO J. 17:5974-5986(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001875; DED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00031; DED; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01335; DED; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
                                                                                               the nucleolus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Blood;
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                                                                                                                                                                                                                                                                                                                               Pan G.
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D -> GEBIQGFORWSRLEGEYKELLGHWAVYAIQY (IN ISOFORM 2).
                                                                                                     Gaps
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                                                                     Ouery Match 14.5%; Score 40; DB 1; Length 318; Best Local Similarity 33.3%; Pred. No. 24; Matches 7; Conservative 8; Mismatches 2; Indels
                              P -> L (IN REF. 5).
FF9D5FF9B61F6BB6 CRC64;
                                                                                                                                                                                                        8, 2002, 19:27:09
                                                                                                                                                               260 WRDYINGSLLEALKGVFITDS 280
                                             36794 MW;
                                                                                                                                  57 WK----GSVVDSVXGVFLTQN 73
   194
                                                                                                                                                                                                         Search completed: November Job time: 5.23529 secs
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318 AA;
   194
                                             SEQUENCE
   VARSPLIC
                              CONFLICT
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211 AA
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MGD; MGT:1892955, Cladn7.
InterPro; IPR001832; Claudin.
InterPro; IPR004031; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin.
PRINTS; PR01077; CLADDIN.
PROSITE; PS01346; CLADDIN: 1.
Tight junction; Transmembrane.
  PRT;
                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-99110921; PubMed-9892664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF087825; AAD09760.1; -.
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22359 MW;
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  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102
                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                     Strausberg R
  CLD7_MOUSE
Q9Z261;
                                                                       Claudin-7.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                   Gaps
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                                                                                                                                                     Score 41; DB 1; Length 1391;
Pred. No. 78;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.5%; Score 40; DB 1; Length 191; 24.4%; Pred. No. 14;
                 HSSP; Q9KWU7; 1HQM.
InterPro; IPR001572; RNA_pol_B.
Pfam; PF00562; RNA_pol_B: 1.
Transferase; Transcription; DNA-directed RNA polymerase; Complete proteome.
SEQUENCE 1391 AA: 15527 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83B445908DFFF41A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 GPAIFIGWAGSALVLLGGALLSCSCPGSESKAAYRAPRSYP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 GXRXFXXWKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                            191 AA
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send an email to license@isb-sib.ch)
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InterPro; IPR004031; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO1077; CLAUDIN.
PROSITE; PS01346; CLAUDIN; 1.
Tight junction; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20366 MW;
                                                                                                                                                     14.9%;
64.3%;
                                                                                                                                       Query Match
Best Local Similarity 64.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                     118 KNSATSSVDGVFLT 131
                                                                                                                                                                                                            58 KGSVVDSVXGVFLT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161
                                                                                                                                                                                                                                                                                                                                                                                Claudin-7 (Fragment).
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100
141
191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                       Morita K., Furuse M., Fujimoto K., Tsukita S.; "Claudin multigene family encoding four-transmembrane domain protein components of tight junction strands "; Proc. Natl. Acad. Sci. U.S.A. 96:511-516(1999).
                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain-
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75618, 056037;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2012 (Rel. 41, Last annotation update)
containing testicular molecule) (DEDProl) (FLDED-1) (KE05).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. 4FE87F3A57AC9F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 GPAIFIGWAGSALVLLGGALLSCSCPGSESKAAYRAPRSYP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 GXRXFXXWKGSVVDSVXGVFLTQNXDXXSSXAXMXXAXXFP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.5%; Score 40; DB 1; 24.4%; Pred. No. 16;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
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SEQUENCE Query Match

Matches

RESULT 14 CLD7\_MOUSE

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Herrmann R.;
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NP_BIND
DOMAIN
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                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license gireement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peterson M.D., Novak K.D., Reedy M.C., Ruman J.I., Titus M.A.;
"Molecular genetic analysis of myoc, a Dictyostelium myosin I.";
J. Cell Sci. 108:1093-1103(1995).
-!- FUNCTION: MYOSIN IS A PROPEIN THAT BINDS TO ACTIN & HAS ATPASE
ACTIVITY THAT IS ACTIVATED BY ACTIN.
-!- SUBUNIT: MYOSIN I HEAVY CHAIN IS SINGLE-HEADED. DIMER OF A HEAV
AND A LIGHT CHAIN. INABILITY TO SELF-ASSEMBLE INTO FILAMENTS.
-!- SIMILARITY: CONPAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                               Nature 39:249-256(1997).
--- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
--- SIMILARITY: BELONGS TO THE UPF0053 FAMILY.
--- SIMILARITY: CONTAINS 2 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 1; Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; CBS domain; Repeat; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E3A0F57ABE8FB323 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1181 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-AX2;
MEDLINE-95348228; PubMed-7622596;
                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y14082; CAA74500.1; -.
EMBL; Z99109; CAB12794.1; -.
Subtilist; BG13022; yhdP.
InterPro; IPR000644; CBS_domain.
InterPro; IPR005170; CorC_HlyC.
InterPro; IPR002550; DUF21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00571; CBS; 2.
Pfam; PF01595; DUF21; 1.
Pfam; PF03471; CorC_H1yC; 1.
SMART; SM00116; CBS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 VDSVXGVFLTQNXD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myosin IC heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444 AA;
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RRARE REPAIR OF THE REPAIR OF 
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBSTRATES.
-:- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit).
RPOB OR MPN516 OR MP326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 1; Length 1181; Pred. No. 66; 9; Indels ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50002; SH3; 1.
Myosin; Actin-binding; AFP-binding; Chemotaxis; SH3 domain; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132915 MW; 5EB1EE47F0CA8803 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON ALPHA-HELICAL, ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1391 AA
                                                                                                                                                                    DictyDP, DD01090; myoC.
InterPro; IPR001609; myoC.
InterPro; IPR001609; myosin_head.
Pfam; PF00018; SH3; 1.
Pfam; PF00018; myosin_head; 2.
PRINTS; PR00193; myoSin_head; 2.
PRINTS; PR00193; myoSin_head; 2.
ProDom; PD000056; SH3; 1.
ProDom; PD000056; SH3; 1.
ProDom; P0000352; myosin_head; 1.
SMART; SM00242; MYSC; 1.
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STRAIN=ATCC 29342 / M129;
MEDLINE-97105885; Pubmed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.9%;
                                                                                                              EMBL; L35323; AAC37427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1181
116
1181
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1181 AA;
                                                                                                                                                    1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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WAS CORRECTED IN POSITION 57.
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Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schlachch S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorkin A., Tacconi E., Takagi T., Takhashi H., Tahkenaru K., Takeuchi M., Tamakoshi A., Tanaar T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Wannutt R., Wedler E., Redler H., Waltzenegger T., Yata K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: SPECIFICALLY METHYLATES THE GUANOSINE IN POSITION 1207 OF 16S RRNA IN THE 30S PARTICLE (BY SIMILARITY).
CATALYTIC ACTIVITY: S-adenosyl-L-methionine + IRNA = S-adenosyl-L-homocysteine + IRNA containing N(2)-methylguanine.
                                                                                                                                                                                                                                                                        "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A POTENTIAL FRAMESHIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
81bosomal RNA small subunit methyltransferase C (EC 2.1.1.52) (rRNA (quanine-N(2)-)-methyltransferase) (165 rRNA m2G1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY. RSMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-TOKYO 1998;
MEDLINE-20445173; PubMed-10993077;
Shigenobu S., Wattanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.9%; Score 41; DB 1; Length 260; 41.7%; Pred. No. 13; Live 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 protein; Complete proteome.
260 AA; 28258 MW; 363B6DDF017BE77E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE UPF0028 (SWS) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Subtilist; BG13363; ylbK.
InterPro; IPR002641; Patatin.
InterPro; IPR001423; UPF0028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01734; Patatin; 1.
PROSITE; PS01237; UPF0028; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 298682; CAB11357.1; -. EMBL; Z99111; CAB13377.1; -.
                                                                                                                                                                                                                                                                                                                          Nature 390:249-256(1997).
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSMC OR BU328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSMC_BUCAI
P57413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
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                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                              EMBL; AP001119; BAB13036.1; ALT_FRAME.
InterPro; IPR002052; N6_Mtase.
InterPro; IPR000051; SAM_bind.
InterPro; IPR000092; N6_MTASE; UNKNOWN_1.
FROSITE; PS00092; N6_MTASE; UNKNOWN_1.
FRIMA Processing; Transferase; Methyltransferase; Complete proteome.
SEQUENCE 338 AA; 39105 MW; E43516DDD22FA014 CRC64;
                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S., Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                  Length 338;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                l; DB 1;
). 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                  Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98044033; PubMed-9384377;
                                                                                                                                                                                                                                                                                                                                                                                WKNLIIKSLPGVFGHKKIDSGS 186
                                                                                                                                                                                                                                                                                                                                                         57 WKGSVVDSVXGVFLTQNXDXXS 78
                                                                                                                                                                                                                                                                                14.98;
                                                                                                                                                                                                                                                                                                   36.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein yhdP
                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YHDP_BACSU
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SPECIES-Phage phi-29;
MEDLINE-66165872; PubMed-3007295;
Garvey K.J., Yoshikawa H., Ito J.;
"The complete sequence of the Bacillus phage phi 29 right early
  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLBK_BACSU 034731;
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                                                                                                                    region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLBK_BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Benes V., Arnold L., Smrt J., Paces V.; "Nucleotide sequence of the right early region of Bacillus phage phi 15 and comparison with related phages: reorganization of gene 17 during evolution."; Gene 75:341-347(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-Phage PZA;
MEDLIAR-87031575; PubMed-3095189;
Paces V. Vlock C. Urbanek P., Hostomsky 2.;
"Nucleotide sequence of the right early region of Bacillus subtilis phage PZA completes the 19366-bp sequence of PZA genome. Comparison with the homologous sequence of phage phi 29.";
Gene 44:115-120(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
-i- INDUCTION: Highest expression in darkness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6D9CFC6C2C2395BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                 EMBL; AF118858; AAG11397.1; ...
InterPro; IPR001905; Ammonium_transp. 1.
TIGRPAMS; TIGR00836; ant; 1.
TIGRPAMS; TIGR00836; ant; 1.
Transport; Transmembrane; Multigene family.
15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 17;
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MEDLINE=89232766; PubMed=2497055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA sphi-29-like viruses.
NCBI_TaxID=10757, 10755, 10756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1988 (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49652 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.98;
                                             TRANSPORTERS (TC 2.49).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage phi-15, and Bacteriophage phi-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 WKGSVVDSVXGVFL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 WEASVTDSINAIYL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1988 (Rel. 08, 01-NOV-1990 (Rel. 16, Early protein GP16.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriophage PZA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VG69_BPPZA
P08388;
                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
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TRANSMEM
TRANSMEM
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A borriss R., Boursier L., Brans A., Brann M., Brignell S.C., Bron S.,
Broulllet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
A brian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A Fritz C., Fujita M., Fujita Y., Fuma S., Gallacin N.,
Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Chiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
A Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bertero M., Presecan E., Glaser P., Richou A., Danchin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.9%; Score 41; DB 1; Length 108; 35.0%; Pred. No. 5.3; ive 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Bacillus subtilis chromosomal region downstream nprE."; Submitted (AUG-1997) to the {\tt EMBL/GenBank/DDBJ} databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AA; 12648 MW; 4FA9C051B60CD8F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein ylbK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                             EMBL; M1813; AAA88498.1; --
EMBL; M28830; AAA32330.1; --
EMBL; M14430; AAA88350.1; --
PIR; E29004; WRBP69.
PIR; JS0193; WRBP13.
PIR; JN0031; JN0031.
Early protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 RXFXXWKGSVVDSVXGVFLT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 RRFASWSGQLLEGSNSVFWT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 35.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
Gene 40:301-309(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1423;
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Spindlin homolog (Protein DXF34). DXF34.
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                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                 Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AT13_LYCES
Q9FVNO;
                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
MOD_RES
CONFLICT
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                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: Tricarboxylic acid cycle.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
-!- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PROD493; CITRATE_SYNTHASE; 1.

Lyase; Tricarboxylic acid cycle; Mitochondrion; Transit peptide.

TRANSIT 7 475 MITOCHONDRION (BY SIMILARITY).

ACT_SITE 310 310 BY SIMILARITY.

ACT_SITE 356 385 BY SIMILARITY.

ACT_SITE 411 411 BY SIMILARITY.

SEQUENCE 475 AA; 52153 MW; F93525B3F31FCB3F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                           Oshida Y., Miyake K., Kanayama S., Kirimura K., Usami S.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Citrate + COA = acetyl-COA + H(2)0
DB 1; Length 474;
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 1; Length 475; Pred. No. 12;
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                             01-00T-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Citrate synthase, mitochondrial precursor (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                             CAPABLE OF OXIDATIVE METABOLISM.
SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPIH_HUMAN STANDARD; PRT; 232 AA. 099865, 075650; Q9UJU0; 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                475 AA
                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002020; Citrate_synt.
                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00285; citrate_s
PRINTS; PR00143; citrate_synt; 1
PROSITE; PS00480; CITRATE SVNT
15.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D63376; BAA09691.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.6%;
58.3%;
                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                               STANDARD;
                                                          |:|||:|| |:
89 WEGSVLDSEEGI 100
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89 WEGSVLDSEEGI 100
                                           57 WKGSVVDSVXGV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                             Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WKGSVVDSVXGV
                                                                                                                                                                                                                                                                                                                                  oxaloacetate.
                                                                                                                                                                                                                                               NCBI_TaxID=5061;
                                                                                                                                                                                                                                                                                 STRAIN-WU-2223L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P23007;
                                                                                                                             CISY_ASPNG
P51044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
SPIH_HUMAN
ID SPIH_HU
AC 099865,
DT 01-NOV-
DT 16-OCT-
                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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-i- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-i- TISSUE SPECIFICITY: Leaves.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots; Asteridae, euasterida I; Solanales; Solanaceae; Solanum.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                    MEDLINE-97419273; PubMed-9271673;
Laval S.H., Reed V., Blair H.J., Boyd Y.;
"The Structure of DXF34, a human X-linked sequence family with
homology to a transcribed mouse Y-linked repeat.";
Mamm. Genome 8:689-691(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C -> R (IN REF. 2).
T -> A (IN REF. 2; CAA18149).
093E7E9F5340BF71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases-1-SIMILARITY: BELONGS TO THE SPIN / STSY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation; Cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ammonium transporter 1, member 3 (LeAMT1;3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION
PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AL022157; CAA18148.1; -. EMBL, A4022157; CAA18149.1; -. InterPro; IPR003671; Spin.Ssty. Pfam; PF02513; Spin.Ssty; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26536 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGXRXFXXWKGSVVDSV 65
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Matches 7; Conservative
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196 196
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HSSP; P23007;
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000098;
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ACT_SITE
SEQUENCE
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                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ueda M., Sanuki S., Kawachi H., Shimizu K., Atomi H., Tanaka A.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Citrate + CoA = acetyl-CoA + H(2)0 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: Tricarboxylic acid cycle.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
          -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE UPF0053 FAMILY.
-!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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Pred. No. 2.2;
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                                                                                                                                                                                                                                                                Pfam; PF03471; CorC_H1yC; 1.
Hypothetical protein; CBS domain; Repeat; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Citrate synthase, mitochondrial precursor (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                              POTENTIAL.
E2EA41573549DA83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467 AA
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                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                        17.1%; Scc.
50.0%; Pred
2;
                                                                                                                                                                                    Subtilist; BG11695; YqhB.
InterPro; IPR000644; CBS_domain.
InterPro; IPR002510; CorC_HlyC.
InterPro; IPR002550; DUF21.
Pfam; PF00571; CBS; 2.
Pfam; PF01595; DUF21; 1.
                                                                                                                                                                                                                                                                                                                                            MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 35, Created)
(Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB001565; BAA19410.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                              396 VDTLGGWFLTQNIDAEPESA 415
                                                                                                                                                              EMBL; D84432; BAA12531.1; -. EMBL; Z99116; CAB14406.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      VDSVXGVFLTQNXDXXSSXA 81
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49956 N
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                                                                                                                                                                                                                                                                                                                                            442 AA;
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TRANSMEM 16
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P79024;
                                                                                                                                                                                                                                                                                                                             TRANSMEM SEQUENCE
                                                                                                                                                                                                                                                                                                                    RANSMEM
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-!- SUBCELLUIAR LOCATION: Mitochondrial matrix.
-!- SUBCELLUIAR LOCATION: Mitochondrial matrix.
-!- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
CAPABLE OF OXIDATIVE METABOLISM.
-!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
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TRANSIT 1 35 MITOCHONDRION (POTENTIAL).
CHAIN 36 474 CITRATE SYNTHASE.
ACT_SITE 310 310 BY SIMILARITY.
ACT_SITE 356 BY SIMILARITY.
ACT_SITE 411 411 BY SIMILARITY.
                                                                                                                 Lyase; Tricarboxylic acid cycle; Mitochondrion; Transit peptide. TRANSIT 1 ? MITOCHONDRION (POTENTIAL). CHAIN ? 467 CITRATE SYNTHASE.
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Eurotiales; Trichocomaceae; Emericella.
NCBL_TaxID=5072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Park B.W., Han K.H., Lee C.Y., Lee C.H., Maeng P.J.; "Cloning and characterization of the citA gene encoding the mitochondrial citrate synthase of Aspergillus nidulans."; mol. Cells 7:290-295(1997).
                                                                                                                                                                                                                                                                                                                                     Score 43; DB 1; Length 467;
                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Citrate synthase, mitochondrial precursor (EC 4.1.3.7).
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BY SIMILARITY.
BY SIMILARITY.
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Pfam; PF00285; citrate_synt; 1.
PRINYS; PR00143; CITRTSNTHASE
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
InterPro; IPR002020; Citrate_synt.
Pfam; PF00285; citrate_synt, 1.
PRINTS; PR00143; CITRTSWIHASE.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
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MEDLINE=97306446; PubMed=9163747;
                                                                                                                                                                                                                                                                                   52004 MW;
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                                                                                                                                                                                                                                                                                                                                     15.6%;
50.0%;
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Best Local Similarity 50.0
Matches 6; Conservative
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301
347
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79 WEGSVLDPIEGI 90
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467 AA;
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310
356
411
474 AA;
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 8, 2002, 19:24:14; Search time 3.23529 Seconds (without alignments) 1153.796 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-840-743-71 275 1 KVXXDXXTXXXWXXLXXXXD.....TQNXDXXSSXAXMXXAXXFP 90

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

YQHB_BACSU   P54505   CISY_CANTR   P799024   CISY_CANTR   P799034   CISY_CANTR   P799094   CISY_CANTR   CISY_CANT	Result No. Sc	Score	% Query Match	Length	DB	SUMMARIES ID	Description
43         15.6         467         1 CISY_CANTR         P79024           43         15.6         474         1 CISY_CANTR         P79024           43         15.6         474         1 CISY_CANTR         P79024           42         15.3         460         1 AT13_LYCES         P69464           41         14.9         108         1 VG69_BPPZA         P694838           41         14.9         108         1 VLBK_BACSU         P674713           41         14.9         181         1 YHDP_BACSU         P675413           41         14.9         1181         1 YHDP_BACSU         P07585           40         14.5         1181         1 XHDP_BACSU         P07585           40         14.5         1391         1 XHDP_BACSU         P07585           40         14.5         1391         1 RPOB_MYCPN         P07513           40         14.5         131         1 DEDD_HUMAN         P07514           40         14.5         318         1 DEDD_HUMAN         P07518           40         14.5         318         1 DEDD_HUMAN         P07514           40         14.5         318         1 DEDD_HUMAN         P07514 <th>1</th> <th>47</th> <th>17.1</th> <th>442</th> <th>-</th> <th></th> <th>DSASOR backling on</th>	1	47	17.1	442	-		DSASOR backling on
43         15.6         474         1 CISY_ERRNI         000098           43         15.6         475         1 CISY_ASPNG         000098           42         15.3         460         1 AT13_LIYCES         091606           41         14.9         108         1 VG69_BPPZA         091701           41         14.9         108         1 VG69_BPPZA         097808           41         14.9         118         1 VG69_BPPZA         097808           41         14.9         118         1 NYSC_DICDI         P67431           40         14.5         1391         1 RPOB_MYCPN         P78013           40         14.5         131         1 RPOB_MYCPN         P78013           40         14.5         318         1 DEDD_MOUSE         092211           40         14.5         318         1 DEDD_MOUSE         09221           40         14.5         318         1 RRPG_LIMAN         0922		43		9	٠,	CISY CANTR	candida t
43         15.6         475         1 CISY_ASPNG         P51044           42         15.3         23.1         SPH_UMAN         Q99865           42         15.3         23.2         1 SPH_UMAN         Q95406           41         14.9         108         1 VG6_BPPZA         Q95401           41         14.9         23.8         1 RYBK_BACSU         P674731           41         14.9         31.8         1 RYBC_BACSU         P674731           40         14.5         1181         1 WYBC_BACSU         P67513           40         14.5         1391         1 CLD7_RAT         Q92711           40         14.5         211         1 CLD7_MOUSE         Q92761           40         14.5         31.8         1 DEDD_HUMAN         Q52761           40         14.5         31.8         1 DEDD_RAT         Q92761           40         14.5         31.8         1 DEDD_RAT         Q92761           40         14.5         31.8         1 DEDD_RAT         Q92761           40         14.5         31.8         1 DED_LWAND         Q92761           40         14.5         31.1         1 ARPG_HUMAN         Q92761 <t< td=""><td></td><td>43</td><td>15.6</td><td>47</td><td>-</td><td>CISY_EMENI</td><td>emericel</td></t<>		43	15.6	47	-	CISY_EMENI	emericel
42         15.3         232         1 SPIH HUMAN         099865           42         15.3         460         1 ATJ_LYCES         09965           41         14.9         108         1 VG69_BPPZA         098138           41         14.9         260         1 YLBK_BACSU         07565           41         14.9         138         1 KSKC_BICAI         07564           41         14.9         1181         1 WYSC_DICDI         P7522           40         14.5         131         1 RNBC_MYCPN         P7622           40         14.5         318         1 DEDD_MOUSE         092211           40         14.5         318         1 DEDD_MOUSE         092221           40         14.5         318         1 DEDD_MOUSE         092261           40         14.5         318         1 DEDD_MOUSE         092261           40         14.5         318         1 DEDD_MOUSE         092261           40         14.5         360         1 CISY_NEUCR         092261           40         14.5         360         1 CISY_NEUCR         092261           40         14.5         360         1 CISY_NEUCR         01003		43		475	٦	CISY_ASPNG	
42 15.3 460 1 AT13 LYCES 994700 41 14.9 108 1 VG69_BPPZA PSZA POR318 41 14.9 260 1 YLBK_BACSU 034713 41 14.9 148 1 1 WYG9_BPZA 007585 41 14.9 148 1 1 MYSC_DICDI P57413 40 14.5 1391 1 MYSC_DICDI P78013 40 14.5 211 1 CLD7_MOUSE 0922611 40 14.5 318 1 DEDD_HUMAN 022611 40 14.5 318 1 DEDD_HUMAN 022611 40 14.5 469 1 CISY_NEUCR 092261 40 14.5 469 1 CISY_NEUCR 092261 40 14.5 796 1 YKST_CABEL 001003 40 14.5 1503 1 MRPC_HUMAN 095255 40 14.5 1503 1 MRPC_HUMAN 099996 39 14.2 208 1 CISY_MATH 099147 39 14.2 240 1 SPIN_MOUSE 061142 39 14.2 270 1 YES3_AQUAE 067438 39 14.2 373 1 DP3B_MYCPU 013336		42		7	1	SPIH_HUMAN	
41         14.9         108         1 VGG9_BPPZA         P08388           41         14.9         260         1 YERK_BACSU         O34731           41         14.9         338         1 RSMC_BUCAI         P07585           41         14.9         1391         1 RYSC_DICDI         P47813           40         14.5         1391         1 RPOB_MYCPN         P78013           40         14.5         21         1 CLD7_RAT         Q92711           40         14.5         318         1 DEDD_MOUSE         Q92761           40         14.5         360         1 CHPL_SCHEC         Q10103           40         14.5         360         1 CHPL_SCHEC         Q10103           40         14.5         391         1 ARPG_HUMAN         Q9278 <t< td=""><td></td><td>42</td><td>•</td><td>4</td><td>٦</td><td>AT13_LYCES</td><td>lycop</td></t<>		42	•	4	٦	AT13_LYCES	lycop
41         14.9         260         1 YLBK BACSU         034731           41         14.9         338         1 RSMC_BUCAI         P57413           41         14.9         1381         1 RMC_DICAI         P75713           41         14.9         1381         1 RPOB_MYCPN         P78013           40         14.5         131         1 CLD7_MOUSE         P78013           40         14.5         318         1 DEDD_MOUSE         O92261           40         14.5         318         1 DEDD_RAT         O92211           40         14.5         318         1 DEDD_RAT         O92211           40         14.5         318         1 DEDD_RAT         O92211           40         14.5         360         1 CISY_NEUCR         P3408           40         14.5         360         1 CISY_NEUCR         P3408           40         14.5         360         1 CIPY_GAPA         O95255           40         14.5         15.01         NRP6_HUMAN         O95255           40         14.5         3911         NRP6_HUMAN         O95955           39         14.2         24.0         SPIN_MOUSE         O61142	_	41	•		-	VG69_BPPZA	
41         14.9         338         1 RSMC_BUCAI         P57413           41         14.9         144         1 KUDP_BACSU         007585           41         14.9         1481         1 MYSC_DICDI         P42521           40         14.5         1391         1 RPOB_MYCPN         P78013           40         14.5         211         1 CLDMOUSE         0922611           40         14.5         318         1 DEDD_HUMAN         075618           40         14.5         318         1 DEDD_HUMAN         092261           40         14.5         318         1 DEDD_HUMAN         09522K           40         14.5         36         1 CISY_NEUCR         0922K           40         14.5         36         1 CISY_NEUCR         09022K           40         14.5         36         1 CISY_NEWAR         089255           40         14.5         164         1 AY46_AMASP         089471	_	41			-	YLBK_BACSU	
41         14.9         444         1 Y HDP_BACSU         007585           41         14.9         1181         1 MYBC_BACSU         007585           41         14.9         1181         1 MYSC_DICDI         P42522           40         14.5         131         1 CLD7_RAT         092111           40         14.5         318         1 DEDD_MOUSE         092261           40         14.5         318         1 DEDD_MOUSE         092261           40         14.5         318         1 DEDD_MOUSE         092261           40         14.5         318         1 DEDD_MOUSE         092286           40         14.5         318         1 DEDD_MOUSE         092286           40         14.5         348         1 DEDD_MOUSE         092286           40         14.5         348         1 DEDD_MOUSE         092286           40         14.5         360         1 CHP1_SCHPO         0910103           40         14.5         351         1 AKP6_LHOMAN         099996           39:5         14.4         164         1 AKP6_LHOMAN         091017           39         14.2         237         1 SPIN_MOUSE         061142 <td>•</td> <td>41</td> <td>•</td> <td></td> <td>7</td> <td>RSMC_BUCAI</td> <td>P57413 buchnera ap</td>	•	41	•		7	RSMC_BUCAI	P57413 buchnera ap
41         14.9         1181         MYSC_DICDI         P42522           41         14.9         1181         MYSC_DICDI         P42522           40         14.5         131         1 CLD7_RAT         P78013           40         14.5         318         1 DED_MUNSE         O92261           40         14.5         318         1 DED_RAT         O92210           40         14.5         318         1 DED_RAT         O92210           40         14.5         318         1 DED_RAT         O92210           40         14.5         360         1 CHPL_SCHPO         O92210           40         14.5         360         1 CHPL_SCHPO         Q10103           40         14.5         1503         1 MRP6_HUMAN         O95255           40         14.5         391         1 ARPE_STRPN         Q99999           39.5         14.4         164         1 ATPE_STRPN         Q99999           39         14.2         240         1 SPIN_MOUSE         P04142           39         14.2         240         1 SPIN_MOUSE         P04165           39         14.2         270         1 SPIN_MOUSE         P04067	_	41	•		7	YHDP_BACSU	bacillus
41         14.9         1391         1 RPOB_MYCPN         P78013           40         14.5         1391         1 CLD7_RAT         Q92111           40         14.5         211         1 CLD7_MOUSE         Q92211           40         14.5         318         1 DEDD_HUMAN         Q92211           40         14.5         318         1 DEDD_HUMAN         Q92211           40         14.5         469         1 CISY_NEUCR         Q9222K           40         14.5         960         1 CHPL_SCHPO         Q10103           40         14.5         960         1 CHPL_SCHPO         Q01010           40         14.5         1503         1 MRPC_HUMAN         Q95255           40         14.5         1503         1 MRPC_HUMAN         Q99996           39.5         14.4         164         1 ATPE_STRPN         Q999996           39         14.2         230         1 SPIN_MOUSE         Q61147           39         14.2         240         1 SPIN_MOUSE         Q61147           39         14.2         268         1 COX3_SCHCO         Q61417           39         14.2         270         1 YES3_AQUAE         Q61414	_	41	•		Н	MYSC_DICDI	
40         14.5         191         1 CLD7_RAT         092111           40         14.5         318         1 DEDD_HUMAN         075618           40         14.5         318         1 DEDD_MOUSE         092113           40         14.5         34         1 CISY NEUCR         092218           40         14.5         796         1 KRST_CAREL         010003           40         14.5         150         1 CHPL SCHPO         010103           40         14.5         150         1 KRPC_HUMAN         09525           40         14.5         1526         1 YY46_ANAP         099996           39         14.2         237         1 SPIN_HUMAN         099967           39         14.2         237         1 SPIN_HUMAN         091417           39         14.2         240         1 SPIN_MOUSE         061142           39         14.2         240         1 YES3_AQUAE         06143	~	41	•		Н	RPOB_MYCPN	
40         14.5         211         1 CLD7_MOUSE         092261           40         14.5         318         1 DEDD_MOUSE         07518           40         14.5         318         1 DEDD_RAT         092261           40         14.5         318         1 DEDD_RAT         0922K0           40         14.5         346         1 CISY_REUCR         P34085           40         14.5         960         1 CHPI_SCHPO         010003           40         14.5         1503         1 MRPG_HUMAN         09525           40         14.5         1520         1 XPAS_HUMAN         09995           39.5         14.4         164         1 ATPE_STRPN         09999           39         14.2         237         1 SPIN_MOUSE         061417           39         14.2         240         1 SPIN_MOUSE         061442           39         14.2         270         1 YES3_AQUAE         061442           39         14.2         270         1 YES3_AQUAE         06142           39         14.2         313         1 BAG_STRPL         06142           39         14.2         313         1 DP3B_MYCPU         06142	~	40	•		Н	CLD7_RAT	
40         14.5         318         1         DEDD_HUMAN         075618           40         14.5         318         1         DEDD_HAT         0922k0           40         14.5         36         1         CISY_NEUCR         0922k0           40         14.5         96         1         CISY_NEUCR         01003           40         14.5         96         1         CHP1_SCHPC         010103           40         14.5         1503         1         MRP6_HUMAN         095255           40         14.5         3911         1         AY46_AMSP         Q89996           39.5         14.4         164         1         ATPE_STRPN         Q99996           39         14.2         208         1         130_ARATH         Q99996           39         14.2         240         1         SPIN_MOUSE         Q61142           39         14.2         240         1         SPIN_MOUSE         Q61142           39         14.2         270         1         YES3_AQUAE         Q66143           39         14.2         313         1         BAG_STRPL         P653257           39         14.2		40	•		7	CLD7_MOUSE	mus m
40         14.5         318         1 DEDD_MOUSE         Q92113           40         14.5         318         1 DEDD_MAT         Q922k0           40         14.5         469         1 CISY_NEUCR         P34003           40         14.5         960         1 CHPI_SCHPO         Q10003           40         14.5         1526         1 YY46_MARN         Q95100           40         14.5         3911         1 ARPS_HUMAN         Q9995           39.5         14.4         164         1 ATPS_ESTRPN         Q9999           39         14.2         237         1 SPIN_HUMAN         Q99657           39         14.2         240         1 SPIN_MOUSE         Q61142           39         14.2         240         1 SPIN_MOUSE         P01418           39         14.2         240         1 SPIN_MOUSE         P04067           39         14.2         270         1 YES3_AQUAR         O6142           39         14.2         313         1 EBAG_STRPL         P04067           39         14.2         313         1 DP3B_MYCPU         Q99RF6           39         14.2         373         1 DP3B_MYCPU         Q99RF6      <		40	•		7	DEDD_HUMAN	075618 homo sapien
40         14.5         318         1         DEDD_RAT         0922KO           40         14.5         469         1         CAST_NEUCR         P34085           40         14.5         150         1         YRS7_CAREL         Q10103           40         14.5         150         1         CHPI_SCHPO         Q10103           40         14.5         1526         1         YY46_ANASP         Q89711           40         14.5         3911         1         ARPE_STRPN         Q99911           39         14.2         20         1         C130_ARATH         Q99652           39         14.2         237         1         SPIN_MOUSE         Q61417           39         14.2         240         1         SPIN_MOUSE         P1418           39         14.2         270         1         YE53_AQUAE         O61418           39         14.2         313         EBAG_STRPL         P04067           39         14.2         313         1         P22A         P04067           39         14.2         313         1         PD3B_MYCPU         Q99RKG           39         14.2         31 <td< td=""><td></td><td>40</td><td>•</td><td></td><td>7</td><td>DEDD_MOUSE</td><td>mus m</td></td<>		40	•		7	DEDD_MOUSE	mus m
40         14.5         469         1 CISY_NEUCR         P34085           40         14.5         796         1 KS7_CAEEL         Q10003           40         14.5         1503         1 MRP6_HUMAN         Q95255           40         14.5         1503         1 MRP6_HUMAN         Q95255           40         14.5         3911         1 AKA9_HUMAN         Q85957           39.5         14.4         164         1 ATPE_STRPN         Q59956           39         14.2         237         1 SPIN_MOUSE         Q61417           39         14.2         240         1 SPIN_MOUSE         Q61142           39         14.2         270         1 YES3_AQUAE         Q61442           39         14.2         270         1 YES3_AQUAE         Q61485           39         14.2         313         1 EBAC_STRPL         Q61485           39         14.2         313         1 DP3B_MYCPU         Q69465           39         14.2         373         1 DP3B_MYCPU         Q98FK6           39         14.2         373         1 DP3B_MYCPU         Q98FK6           39         14.2         373         1 DY1_HUMAN         Q13336  <		40	•		н	DEDD_RAT	Q922k0 rattus norv
40         14.5         796         1 YRS7 CAEEL         Q10003           40         14.5         960         1 CHPL_SCHPO         Q10103           40         14.5         1526         1 YY46_ANASP         Q8711           40         14.5         3911         1 AKA9_HUMAN         Q89996           39.5         14.4         16.4         1 AKPF_STRPN         Q89996           39         14.2         208         1 C130_ARATH         Q99657           39         14.2         237         1 SPIN_HUMAN         Q99657           39         14.2         240         1 SPIN_MOUSE         Q61142           39         14.2         26         1 CNS_AS_CHCO         P014057           39         14.2         270         1 YES_AQUAE         O67438           39         14.2         313         1 EBAG_STRPL         P04067           39         14.2         373         1 DPPB_MYCPU         Q99RFG           39         14.2         373         1 DPPB_MYCPU         Q99RFG           39         14.2         373         1 UT1_HUMAN         Q13336		40	•		-	CISY_NEUCR	P34085 neurospora
40         14.5         960         1         CHPL_SCHPO         Q10103           40         14.5         1503         1         WRPG_HUMAN         095255           40         14.5         1526         1         YY46_ANASP         Q89yril           39.5         14.4         164         1         AFF_STRPN         Q99996           39         14.2         208         1         C130_ARATH         Q91967           39         14.2         237         1         SPIN_HUMAN         Q91637           39         14.2         240         1         SPIN_MOUSE         Q61142           39         14.2         270         1         YE53_AQUAE         O67438           39         14.2         313         1         BAG_STRPL         P04067           39         14.2         313         1         P1402         P04067           39         14.2         373         1         DP3B_MYCPU         Q99RK6           39         14.2         373         1         DP3B_MYCPU         Q99RK6           39         14.2         389         1         U11_HUMAN         Q13336		40			<del>, - 1</del>	YRS7_CAEEL	Q10003 caenorhabdi
40         14.5         1503         1         MRP6 HUMAN         095255           40         14.5         15.6         1         Y46_ANASP         Q8Yf11           40         14.5         3911         1         ARA9_HUMAN         Q99g51           39.5         14.4         164         1         ATPE_STRPN         Q5952           39         14.2         237         1         SPIN_HUMAN         Q99657           39         14.2         240         1         SPIN_MOUSE         Q61142           39         14.2         270         1         YE53_AQUAE         O67438           39         14.2         313         1         EBAC_STRPL         O67438           39         14.2         313         1         P33257         P533257           39         14.2         373         1         PP3B_MYCPU         Q98K6           39         14.2         373         1         PP3B_MYCPU         Q98K6           39         14.2         389         1         V1_LHUMAN         Q13336	_	40			П	CHP1_SCHPO	
40         14.5         1526         1 YY46_ANASP         Q8yrill           39.4         14.5         3911         1 AKA9_UNMAN         Q99996           39.5         14.4         164         164         164         Q9996           39         14.2         237         1 SPIN_HUMAN         Q99657           39         14.2         237         1 SPIN_HUMAN         Q99657           39         14.2         264         1 SPIN_MOUSE         Q61142           39         14.2         26         1 YE53_AQUAE         O67438           39         14.2         31.3         1 EBAG_STRPL         P04067           39         14.2         37.3         1 DP3B_MXCPU         Q98FK6           39         14.2         37.3         1 DP3B_MXCPU         Q98FK6           39         14.2         37.3         1 UT1_HUMAN         Q13336		40	•		Н	MRP6_HUMAN	095255 homo sapien
40         14.5         3911         1 ARA9 HUMAN         099996           39.5         14.4         164         1 ATPE_STRPN         Q59952           39         14.2         208         1 CI30_ARATH         Q91417           39         14.2         237         1 SPIN_MOUSE         Q91617           39         14.2         260         1 COX3_SCHCO         P040657           39         14.2         270         1 YES3_AQUAR         O67438           39         14.2         313         1 EBAG_STRPL         P04067           39         14.2         373         1 DP3B_MYCPU         Q98PK6           39         14.2         373         1 DP3B_MYCPU         Q98PK6           39         14.2         373         1 UT1_HUMAN         Q13336		40	•		-	YY46_ANASP	
39.5 14.4 164 1 ATPE_STRPN 059952 39 14.2 230 1 C130_ARATH 091917 39 14.2 237 1 SPIN_HUMAN 099657 39 14.2 240 1 SPIN_MOUSE 061142 39 14.2 270 1 YE53_AQUAE 067438 39 14.2 313 1 EBAG_STRPL 067438 39 14.2 313 1 DP3B_MYCPU 0998K6 39 14.2 373 1 DP3B_MYCPU 0998K6 39 14.2 373 1 DP3B_MYCPU 0998K6 39 14.2 373 1 DP3B_MYCPU 0988K6		4	•		Н	AKA9_HUMAN	
39 14.2 208 1 CI3O_ARATH Q91Qi7 39 14.2 237 1 SPIN_HUMAN Q9y657 39 14.2 240 1 SPIN_MOUSE Q61142 39 14.2 268 1 COX3_SCHCO P14058 39 14.2 270 1 YE53_AQUAE O67438 39 14.2 313 1 EBAG_STRPL P04067 39 14.2 314 1 GCSSTRPL P04067 39 14.2 373 1 DP3B_MYCPU Q98rK6 39 14.2 373 1 UTI_HUMAN Q13336	m	9.	٠		Н	ATPF_STRPN	Q59952 streptococc
39 14.2 237 1 SPIN HUMAN Q9y657 39 14.2 240 1 SPIN_MOUSE Q61142 39 14.2 268 1 COX3_SCHCO P14058 39 14.2 270 1 YE53_AQUAE O67438 39 14.2 313 1 EBAG_STRPL P04067 39 14.2 373 1 DP3B_MYCPU Q98RK6 39 14.2 373 1 DP3B_MYCPU Q98RK6 39 14.2 389 1 UT1_HUMAN Q13336		39	•		7	CI30_ARATH	Q91qi7 arabidopsis
39 14.2 240 1 SPIN_MOUSE 061142 39 14.2 276 1 COS_SCHCO P14058 39 14.2 270 1 YE53_AQUAE 067438 39 14.2 313 1 EBAG_STRPL P04067 39 14.2 314 1 YG20_YEAST P533257 39 14.2 373 1 DP3B_MYCPU Q98RK6 39 14.2 373 1 UT1_HUMAN Q13336		39	•		-	SPIN_HUMAN	. Q9y657 homo sapien
39 14.2 268 1 COX3_SCHCO P14058 39 14.2 270 1 YE53_AQUAE 067438 39 14.2 314 1 YG2O_YEAST P04067 39 14.2 313 1 DP3B_MYCPU Q98rK6 39 14.2 373 1 DP3B_MYCPU Q98rK6 39 14.2 389 1 UT1_HUMAN Q13336		39	٠		Н	SPIN_MOUSE	
39 14.2 270 1 YE53 AQUAE 067438 39 14.2 313 1 EBAG_STRPL P04067 39 14.2 314 1 YESST PSST P5357 39 14.2 373 1 DP3B_MYCPU Q98rK6 39 14.2 389 1 UT1_HUMAN Q13336		33	٠		Н	COX3_SCHCO	
39 14.2 313 1 EBAG_STRPL P04.067 39 14.2 314 1 YQ2O_LPESST P53257 39 14.2 373 1 DP3B_MYCPU Q98RK6 39 14.2 389 1 UTI_HUMAN Q13336		33	٠		-	YE53_AQUAE	
39 14.2 314 1 YG2O_YEAST P53257 39 14.2 373 1 DP3B_MYCPU Q98rk6 39 14.2 389 1 UT1_HUMAN Q13336		36	•		-	EBAG_STRPL	_
39 14.2 373 1 DP3B_MYCPU Q98rk6 39 14.2 389 1 UT1_HUMAN Q13336		39	٠		Н	YG20_YEAST	7
39 14.2 389 1 UT1_HUMAN Q13336		39	•		7	DP3B_MYCPU	
		39	14.2		7	UT1_HUMAN	

P54428 bacillus su P02675 homo sapien	Q44052 arthrobacte P35315 trypanosoma	P38008 chlamydia t	P42780 bacteroides	P36324 raspberry r	Q9x4w3 vibrio chol Q58254 methanococc	095471 homo sapien	Q9yh92 brachydanio
YRKA_BACSU FIBB HUMAN	IMD_ARTGO	PMPF_CHLTR	BPRX_BACNO	POL2_RRVS	RTXC_VIBCH MCRV_METJA	CLD7_HUMAN	CLDX_BRARE
7	<del></del>	Н.		,	٦,	Н	Т
434	641	1034	595	1107	200	211	215
14.2	14.2	14.2	14.0	14.0	13.8	13.8	13.8
39 39	39 39	39	38.5	38.5	388	38	38
34 35	36 37	38	40	41	4 4 3 8	44	45

# ALIGNMENTS

PACSU (YOHB_BACSU STANDARD; PRT; 442 AA. 1948.05) 194505; 01-0CT-1996 (Rel. 34, Created) 10-0CT-1996 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) HYPOTHETICAL Protein YqhB. Sactilus subtilis. Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	Ill SEQUENCE FROM N.A. STRAIN-168 / JH642; STRAIN-168 / JH642; MIZDIN-297124195; PubMed-8969508; MIZDIN-297124195; PubMed-8969508; MIZDIN-207124105 SAGUENCING Of the 283 kb 210 degrees-232 degrees region of sporulation genes."; Sporulation genes."; MICTODIOLOGY 142:3103-3111(1996).	Parallel Structure From N.A.  STRAIN-168  WEDLINE-98004033; Pubmed-9384377;  WEDLINE-98004033; Pubmed-9384377;  WEDLINE-98004033; Pubmed-9384377;  WEDLINE-98004033; Pubmed-9384377;  Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Dessieres P., Bolotin A., Borchert S., Boursier L., Bruschl C.V., Caldwell B., Capueno V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entingron J., Fabret C., Ferrari E., Foulger D., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Gliser P., Goffeau A., Golightly E.J., Grandi G., Hilbert H., Holsappel S., Haacot J., Harwood C.R., Heamat A., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayershi Y., Koetter P., Kontingstein G., Krogl S., Kumano M., Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C., Medino R., Lovine A., Liu H., Masuda S., Mauel C., Medigue C., Medindo R.D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parce V., Pohl T.M., Porteelle D., Porwollik S., Prescott A.M., Parce O., Pohl T.M., Porteelle D., Porwollik S., Prescott A.M., Seror S.J., Serror P., Shin B.S., Soldo B., Scorion F., Yolic P., Puric P., Puranka T., Takahashi H., Takamaru K., Takakuchi M., Tamakoshi A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tackoni E., Takagi T., Takahashi H., Takemaru K., Varanko H., Wanbutt R., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wassarotti A., Wanbutt R., Wanbutt R., Yamamoto H., Yamane K., Yasumoto K., Yasumoto H., Wanner B., Dacchilla W., Brobellis W., Server B., Brobella M., Wanner B., Dacchilla W., Brobella M., Wanner B., Walle C., Walle M., Walle Lise., Solic B
1	SEQUENCE FROM N.A STRAIN=168 / JH64 MEDLINE-97124195; Mizuno M., Masuda Kobayashi Y.; Systematic seque the Bacillus subt sporulation genes Microbiology 142: [2]	SERVINE-98044 KURST F. Oga AZEVEGO V. B BOTTISS R., B ENTIA R. D., G Ghim S.Y., Gl Ghim S.Y., Lev Medina N., Me Moone D. O'R Parco V., Poh Presecan E., Fleger M., Ri Sato T., Scan Sekiguchi J., Sorokin A., T Takeuchi M., Tosato T., Scan Sekiguchi J., Sorokin A., T Takeuchi M., Tosato T., Wum Winters P., W Tosato A., Wum Winters P., W Tosato A., T Takeuchi M., Tosato A., Wam Winters P., W Tosato A., T Takeuchi M., Tosato A., T T T T T T T T T T T T T T T T T T T
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flowering time; endosperm development; MEDEA.

23-APR-2001; 2001WO-US13059. 21-APR-2000; 2000US-0553690.

WO200180626-A1. Triticum sp.

01-NOV-2001

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                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATRODOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the confrol of a prometra at least 70% identical to DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein. The expression cassette is polynucleotide encoding a DMT-like protein. The expression cassette is polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably adrobacterium by sexual cross, and selecting a host cell preferably in flowering time, introduction of the protein in a plant results in a delay in flowering time, introduction of the protein in a plant results in a delay in flowering time, introduction of the protein in an Arabidopsis leaf results in modulation of methylation of protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. The polynucleotide is useful for detecting a nucleic acid in a sample. The protein of target genes by demethylation. The present sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                 New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
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DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
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DNA demethylation; transgenic plant; transcription modulation;
                                                                                                                                                                                                               Tatarinova TV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.4%; Score 79; DB 23; Length 20
44.2%; Pred. No. 2.3e-08;
tive 0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 KXXXXLRTEHXVXXLPDXHXXLXX-----XDXXXYLLXIWXP 140
                                                                                                                                                                                                               Okamuro JK,
                                                                                                                                                                                                                                                                                                                           Disclosure; Page 90; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU72750 standard; Protein; 108 AA
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                                                                                                                            23-APR-2001; 2001WO-US13059.
                                                                                                                                                      21-APR-2000; 2000US-0553690.
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Matches 19; Conservative
                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                             Choi Y,
                                                                                                                                                                                                                                        WPI; 2002-055307/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wheat DMT3 protein.
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                                                                    WO200180626-A1
                                                                                                                                                                                                            Fischer RL,
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                                        Glycine max
                                                                                                01-NOV-2001
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The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMPER) previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a region of DMT a host cell comprising an exogenous polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of chromosomal DNA in the cell, reduction of expression of the protein in a plant results in a delay in flowering time, introduction of chromosomal DNA in the cell, reduction of expression of the protein in an Arabidopsis leaf results in expression of the protein in a natural of suseful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylotycine glycosylases and regulates
                                                                                                                                                                                                                                                                                 New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
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                                                                              Tatarinova TV;
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Pred. No. 3.1e-08;
0; Mismatches 55
                                                                              Hannon M, Okamuro JK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents a DMT-like protein
                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 87; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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13.1%;
Best Local Similarity 29.5%;
Matches 23; Conservative 0
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(REGC ) UNIV CALIFORNIA
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                                                                              Fischer RL, Choi Y,
                                                                                                                                                             WPI; 2002-055307/07.
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Tatarinova TV;

Okamuro JK,

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New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
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                                                                                                                                                                                                             Hannon M,
                                                 23-APR-2001; 2001WO-US13059.
                                                                                                     21-APR-2000; 2000US-0553690.
                                                                                                                                                   (REGC ) UNIV CALIFORNIA.
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01-NOV-2001
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                                                                                                                                                New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
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                        Tatarinova TV;
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Pred. No. 3.5e-10;
0; Mismatches 112;
                        Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 LXXXXIXXXFXXGXXCXRXFXXXXXXXXX 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents a DMT-like protein.
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                                                                                                                                                                                                                             Disclosure; Page 94; 109pp; English.
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                        Hannon M,
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22.78;
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nes 34; Conservative
                     Choi Y,
                                                                       WPI; 2002-055307/07.
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                                                                                                     N-PSDB; AAS96709
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                     Fischer RL,
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The invention relates to an isolated polynucleotice at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or Complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or C their compliations. Also included are an expression assette comprising the polywuclectide or comprising a heterologus polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence or an 5' untranslated encoding a DMT-like protein. The expression cassette is polynucleotide encoding a DMT-like protein. The expression cassette is polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of chromosomal DNA in the cell, reduction of expression of the protein in a Arabidopsis leaf results in expression of the protein in a plant results in enhanced endosperm development and expressing of the DEMETER is related to 5-methylcytosine glycosylases and regulates

C DEMETER is related to 5-methylcytosine glycosylases and regulates

C DEMETER is related to 5-methylcytosine glycosylases and regulates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 TILVPCRTAMRGSFPLNGTYFQVNEVFADHRSSHNPIHVEREMLWNLQRRMVFFGTSVPT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 DPTPYLLAIWTP--DGIKEITKTPKPC--CDPQMGGDLCNNEMCHNCTAEKENQSRYVRG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1e-09;
0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 IXXXLXXXXIXXXFXXGXXCXRXFXXXXXXXXXXXLXXXLH 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 IFKGLRTEEIQQCFWRGFVCVRGFDMETRAPRPLCPHLH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 85; DB 23;
Pred. No. 1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents a DMT-like protein.
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Matches 37; Conservative
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RESULT 13 AAU72764

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(REGC ) UNIV CALIFORNIA
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New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
                                                                The invention relates to an isolated polynucleotide sequence or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 KXXXXLRTEHXVXXLPDXHXXLXXXDX-----XXYLLXIWXPXXXXXX----XXXXXXX 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 KNVSRLRTEHCVYELPDTHPLLQGWDTREPDDPGKYLLAIWTPGETANSIQPPESKCSSQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 88.5; DB 23; Length 102;
Pred. No. 1e-10;
0; Mismatches 52; Indels 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 EEC------GOLCNENECFSCNSFREANSQIVRGTLL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okamuro JK,
                                       Disclosure; Page 91; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cotton DMT protein related sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU72760 standard; Protein; 137 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                  15.0%;
28.3%;
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Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       102 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% and their compinations. Also included are an expression or c or their combinations. Also included are an expression or C or their combinations. Also included are an expression or C or their combinations. Also included are an expression or C or their combinations. Also included are an expression or DMT, a host cell comprising a percent of a promoter at least 70% identical to DMT, a host cell comprising an exogenous polynucleotide are protein and a transgenic plant comprising a conduing a DMT-like protein. The expression cassette is consisted in a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following bloodical activities, which include enhanced expression of the protein into a cell results in a delay in flowering time, introduction of the protein in an plant results in modulation of methylation of the protein in an hanced endosperm development and expressing of the protein in an handlogous leaf results in expression of the protein in a plant result in explain the cell, reduction of expression of the protein in an handlogous leaf results in expression of the protein in a plant result for detecting a nucleic acid in a sample. The polynucleotide is useful for detecting a nucleic acid in a sample. The polynucleotide a pum-like protein The present
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                                                                                                                            New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 23; Length 137;
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29.8%; Pred. No. 2.9e-10;
tive 0; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 -GSQEPGRLCNEKTCFACNSVREANTETVRGTIL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents a DMT-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corn DMT protein related sequence #1.
                                                                                                                                                                                                                                                     Disclosure; Page 94; 109pp; English.
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2002-055307/07.
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Matches 28; Conserv
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DNA demethylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 AA;
                                           N-PSDB; AAS96710
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RESULT 10
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                                                                                   (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                              1166 ALFESNNTLCNENKCFOCNKTREEESQTVRGTILIPCRTAMRGGFPLNGTYFQTNEVFAD 1225
                                                                                                                                                                                                                                                                                                            1109 KIKEKLRTEHHVFELPDHHSILEGFERREAEDIVPYLLAIWTP-GETVNSIQPPKQRC-- 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40%
                                                                                                                                                                                                                                                                                                                                      104 KXXXXLRTEHXVXXLPDXHXXL-----XXXDXXXXLLXIWXPXXXXXXXXXXXXXXXXXX 157
                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                  DB 23; Length 1309;
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DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tatarinova TV;
                                                 Claim 5; SEQ ID NO 1471; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                HDSSINPIDVPTELIWDLKRRVAYLGSSVSSICKGLSVEAIKYNFQEG 1273
                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to identifying target proteins
                                                                                                                                                                                                                               Score 108.5; DB 23;
Pred. No. 7.6e-14;
0; Mismatches 117;
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                                                                                                                                                                                                                                 18.4%;
25.0%;
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                                                                                                                                                                                                       1309 AA;
                                                                                                                                                                                                                                          Local Similarity
es 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corn DMT1 protein.
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                  or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual
identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 PCRTAMRGSFPLNGTYFQVNEVFADHCSSQNPIDVPRSWIWDLPRRTVYFGTSVPTIFRG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 YLLSIWTP-GETAQSIDAPKTFC---DSGETGRLCGSSTCFSCNNIREMQAQKVRGTLLI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 LTTEEIQRCFWRGFVCVRGFDRTVRAPRPLYARLHFPVSK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 100; DB 23;
Pred. No. 6.3e-13;
0; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU72755 standard; Protein; 102 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-2000; 2000US-0553690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-055307/07.
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Seguence
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protein in a plant results in a delay in flowering time, introduction of the protein into a cell results in modulation of methylation of chromosomal DNA in the cell, reduction of expression of the protein in a plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylcytosine glycosylases and regulates sequence represents a DMT-like protein. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprising a sequence or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DWT (DEWETER, previously known as ATROPOS (ATR)) Domain A, or C or their combinations. Also included are an expression
                                                                                                                                                                                                                                                                                                      HETSLNPIVFRRELCKGLEKRALYCGSTVTSIFKLLDTRRIELCFWTGFLCLRAFDRKQR 1051
                                                                                                                                                                                        KYYNRLRIEHVVYVLPDNHELLHDFERRKLDDPSPYLLAIWQP-GETSSSFVPPKKKC-- 955
                                                                                                                                                                                                                                     Length 1114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide that control plant development having a specific homology to DEMETER domains A,B
                                                                                                                                                                  0; Mismatches 108;
                                                                                                                                                                                                                                                           --SSDGSKLCKIKNCSYCWTIREONSNIFRGTIL-----
                                                                                                                                        ch 22.8%; Score 134.5; DB 3
1 Similarity 25.8%; Pred. No. 1.8e-19,
49; Conservative 0; Mismatches 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tomato DMT protein related sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 92; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                AAU72757 standard; Protein; 210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-2001; 2001WO-US13059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-2000; 2000US-0553690
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                      1052 DPKELVRRLH 1061
                                                                                                                                                                                                                                                                                                                                278 XPXXLXXXLH 287
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                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU72757;
                                                                                                                     Sequence
                                                                                                                                           Query Match
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cassette comprising the polynucleotide or comprising a heterologous bolynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking an exagence or an 5' untranslated region of DMT, a host cell comprising an exagence polynucleotide encoding a DMT-like protein and a transgenic plant comprising a polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following protein in a plant results in a clay in flowering time, introduction of the protein into a cell results in modulation of methylation of the protein in the cell, reduction of expression of the protein in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant results in enhanced endosperm development and expressing of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. DEMETER is related to 5-methylcytosine glycosylases and regulates transcription of target genes by demethylation. The present sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 KXXXXLRTEHXVXXLPDXHXXLXX-----XDXXXYLLXIWXPXXXXXX----XXXXXXX 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DC-----GOLCNEEECFSCNSFREANSQIVRGTILIPCRTAMRGSFPLNGTYFQVNE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 VFADHESSLNPISVPRSLIWNLDRRTVHFGTSVTSIFKGLATPEIQQCFWRGFVCVRSFE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying plant target proteins for herbicidally active compounds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 KNVSRLRTEHSVYELPDSHPLLEGWEKREPDDPGKYLLAIWTPGETANSIQPPDRRCSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 132; DB 23;
Pred. No. 1.1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herbicidally active polypeptide SEQ ID NO 1471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herbicidal; plant; agriculture; herbicide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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24.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FARB ) BAYER AG.
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The invention relates to an isolated polynuclectide sequence or their complement encoding a polypeptide having a sequence at least 40% complement encoding a polypeptide having a sequence at least 40% complement encoding a polynuclesty known as ATRODOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous copynucleotide under the control of a promoter at least 70% identical to DMT 5 flanking sequence, DMT 3 flanking sequence or an 5 untranslated region of DMT, a host cell comprising an exogenous polynucleotide comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a computing transcription. The method comprises introducing useful for modulating transcription. The method comprises introducing cost the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following cross, and selecting a host cell with modulated transcription of the protein in a plant results in a delay in flowering time, introduction of the protein in a plant results in a delay in flowering time, introduction of the protein in a plant results in a delay in flowering time, introduction of chromosomal DNA in the cell, reduction of expression of the protein in an Arabidopsis leaf results in medulation of methylation of protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. ComeMETER is related to 5-methylotosine glycosylases and regulates

C pageunce represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
  -----GQLCNEEECFSCNSFREANSQIVRGTILIPCRTAMRGSFPLNGTYFQVNE 139
                                          140 VFADHESSLNPISVPRSLIWNLDRRTVHFGTSVTSIFKGLATPEIQQCFWRGFVCVRSFE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 71; 109pp; English.
                                                                                                                                                                                                                                                                                AAU72739 standard; Protein; 1332 AA
                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis DMT3 (1DMT3) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-2000; 2000US-0553690
                                                                                                                           274 XXXXXPXXLXXXLHXXXS 291
                                                                                                                                                                        200 RSTRAPRPLMARLHFPAS 217
                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis Thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-055307/07.
N-PSDB; AAS96693.
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The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMPTER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a prometer at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following biological activities, which include enhanced expression of the
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                                                                                                                                                                                                                                                        1249 HDSSINPIDVPTELIWDLKRRVAYLGSSVSSICKGLSVEAIKYNFQEGYVCVRGFDRENR 1308
                                                                                                           1132 KIKEKLRTEHHVFELPDHHSILEGFERREAEDIVPYLLAIWTP-GETVNSIQPPKQRC-- 1188
                                                                                                                                                                                 1189 ALFESNNTLCNENKCFQCNKTREEESQTVRGTILIPCRTAMRGGFPLNGTYFQTNEVFAD 1248
                                                                        Length 1332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Okamuro JK, Tatarinova TV;
                                      Indels
   DB 23;
                                    132;
Score 137.5; DB 2
Pred. No. 4.8e-20;
); Mismatches 132
                                                                                                                                                                                                                                                                                                                                                                                                                           AAU72741 standard; Protein; 1114 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis DMT4 (1DMT4) protein.
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0
   23.3%;
25.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis Thaliana.
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                                                                                                                                                                                                                                                                                                                                 1309 KPKSLVKRLH 1318
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                                                                                                                                                                                                                                                                                              278 XPXXLXXXLH 287
                     Best_Local Similarity
Matches 49; Conserv
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     Query Match
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(first entry)

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New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or C
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DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                            Alfalfa DMT protein related sequence.
                                            AAU72756 standard; Protein; 217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-2001; 2001WO-US13059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-2000; 2000US-0553690.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-055307/07.
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                                                                                                                                                                                                                                                                                                            Medicago sativa.
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                                                                                         AAU72756;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% dentical to DMT (DEMPTER, previously known as ATROPOS (ATR)) Domain A, B control to their combinations. Also included are an expression assette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5. flanking sequence, DMT 3. flanking sequence or an 5. untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein. The expression cassette is useful for modulating transcription. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual useful for modulating at least one of the following the protein is capable of exhibiting at least one of the following bloological activities, which include enhanced expression of the protein in a plant results in a delay in flowering time, introduction of plant results in enhanced endosperm development and expression of the protein in a plant results in enhanced endosperm development and expressing of the protein in an Arabitopsis leaf results in expression of the protein in a plant result for detecting a nucleic acid in a sample. The polynucleotide is useful for detecting a nucleic acid in a sample. The permanent and expression of the protein in a plant results of methylotosine glycosylases and regulates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1745 KNVSRLRTEHQVYELPDSHPLLEGFNQREPDDPCPYLLSIWTP-GETAQSTDAPKSVC-- 1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1861 HDSSRNPIDVPRSWIWNLPRRTVYFGTSIPTIFKGLTTEEIQHCFWRGFVCVRGFDRTSR 1920
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DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 145; DB 23; Length 1952;
Pred. No. 1.8e-21;
0; Mismatches 134; Indels 10
                                                                                                                                                                                                                                                                                                                                 Okamuro JK, Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 79-80; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents a DMT-like protein
                                                                                                                                                                                                                                                                                                                                 Hannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.6%;
                                                                                                                                                                                              23-APR-2001; 2001WO-US13059.
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nes 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1921 APRPLYARLHFPASK 1935
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                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                              Choi Y,
                                                                                                                                                                                                                                                                                                                                                                       2002-055307/07
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                                                                                                           WO200180626-A1.
                                                                 Oryza sativa.
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Matches
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Okamuro JK, Tatarinova TV;

Hannon M,

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The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5 flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a centranslated comprise in the polynucleotide encoding a DMT-like protein. The expression cassette is confounded in the protein and a transgenic plant comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following brotein in a plant results in addition of expression of the protein in a plant results in andulation of methylation of chromosomal DNA in the cell. reduction of expression of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. The polynucleotide is useful for detecting a nucleic acid in a sample. The protein in the present transcription of target genes by demethylation. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 KNVSRLRTEHSVYELPDSHPLLEGWEKREPDDPGKYLLAIWTPGETANSIQPPDRRCSAQ 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.2%; Score 143; DB 23; Length 217; 25.3%; Pred. No. 4.9e-22; Live 0; Mismatches 130; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents a DMT-like protein,
Disclosure; Page 92; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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st Local Sim-
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21-APR-2000; 2000US-0553690
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                                             The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% identical to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B or C or their combinations. Also included are an expression cassette comprising the polynucleotide or comprising a heterologous cassette comprising the polynucleotide or comprising a heterologous polynucleotide under the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated region of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein and a transgenic plant comprising a cencoding a DMT-like protein and a transgenic plant comprising a polynucleotide encoding a DMT-like protein. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably Agrobacterium by sexual cross, and selecting a host cell preferably advobacterium of the following bloogical activities, which include enhanced expression of the protein in a plant results in advolution of methylation of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. Content of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. Content of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1533 KNISRLRTEHQVYELPDSHRLLDGMDKREPDDPSPYLLAIWTP-GETANSAQPPEQKC-- 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1649 HESSLKPIDVPRDWIWDLPRRTVYFGTSVTSIFRGLSTEQIQFCFWKGFVCVRGFEQKTR 1708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 146; DB 23; Length 1729;
Pred. No. 9.6e-22;
0; Mismatches 134; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Demeter; DWT; Atropos; ATR; 5-methylcytosine glycosylase;
DNA demethylation; transgenic plant; transcription modulation;
flowering time; endosperm development; MEDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents a DMT-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU72737 standard; Protein; 1413 AA.
                  Claim 3; Page 54-55; 109pp; English.
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Local Similarity 26.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1729 AA;
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complement encoding a polypeptide having a sequence at least 40% of complement encoding a polypeptide having a sequence at least 40% of complement encoding a polypeptide having a sequence at least 40% of comprising the polynucleotide are an expression cassette comprising the polynucleotide or comprising a heterologous cassette comprising the control of a promoter at least 70% identical to polynucleotide under the control of a promoter at least 70% identical to comprising sequence. DAT 3' flanking sequence or an 5' untranslated region of DAT, a host cell comprising an exogenous polynucleotide encoding a DAT-like protein and a transgenic plant comprising a polynucleotide encoding a DAT-like protein. The expression cassette is copynucleotide encoding a DAT-like protein. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following cross, and selecting a host cell with modulated transcription of the protein in a plant results in a delay in flowering time, introduction of the protein into a not the cell, reduction of expression of the protein in a hand results in modulation of methylation of the protein in an Arabidopsis leaf results in expression of the MEDDRA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. Compensation of transcription of target genes by demethylation. The present compensation of transcription of transcription of marget genes by demethylation. The present
                                                                                                                                                                                                                                                                     New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B\ {\rm or}\ C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1413;
                                                                         Tatarinova TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.6%; Score 145; DB 23; Length 1.
26.2%; Pred. No. 1.3e-21;
Live 0; Mismatches 134; Indels
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                                                                             Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 67; 109pp; English.
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                                                                             Hannon M,
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Matches 51; Conserva
                                                                                                                                                              WPI; 2002-055307/07
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                                                                                 Fischer RL,
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; Search time 45.3268 Seconds (without alignments) 858.415 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Arabidopsis Demete	Arabidopsis DMT2 (	Rice DMT1 protein.	Alfalfa DMT protei	Arabidopsis DMT3 (	Arabidopsis DMT4 (	Tomato DMT protein	Herbicidally activ	Corn DMT1 protein.	Soybean DMT4 prote
SUMMARIES		ΙΩ		AAU72737	AAU72743	AAU72756	AAU72739	AAU72741	AAU72757	ABB92260	AAU72745	AAU72755
		DB	23	23	23	23	23	23	23	23	23	23
		Query Score Match Length DB I	1729	1413	1952	217	1332	1114	210	1309	177	102
	dР	Query Match	24.7	24.6	24.6	24.2	23.3	22.8	22.4	18.4	16.9	15.0
		Score	146	145	145	143	137.5	134.5	132	108.5	100	88.5
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AAU72760 AAU72759 AAU72764 AAU72754	AAU72767 AAU72767 AAU72768 AAU72768	AAU72770 AAU72770 ABB62738 AAB72443 AAM47583	AAY90301 AAU12260 AAM92597 AAM38606	AAM8162 AAM35357 AAU50869 AAY95685 AAU48812 AAU53845	AAY43219 ABB70840 AAB77372 AAQ27373 AAM94749 AAG06711 AAG06710 AAG10493
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137 164 179 209 108	138 150 89 93	1548 1548 1548 1548	223	985 144 204 204 662 75 81	606 1289 49 83 83 109 112 112 152
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## ALIGNMENTS

Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; DNA demethylation; transgenic plant; transcription modulation; flowering time; endosperm development; MEDEA. Tatarinova TV; Okamuro JK, AAU72736 standard; Protein; 1729 AA Fischer RL, Choi Y, Hannon M, Arabidopsis Demeter protein. 23-APR-2001; 2001WO-US13059. 21-APR-2000; 2000US-0553690. WPI; 2002-055307/07. N-PSDB; AAS96686, AAS96689. (first entry) (REGC ) UNIV CALIFORNIA. Arabidopsis Thaliana WO200180626-A1. 26-FEB-2002 01-NOV-2001. AAU72736; AAU72736 RESULT 1 

New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or  ${\tt C}$ 

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Query Match 5.4%; Score 32; DB 1; Length 578; Best Local Similarity 50.0%; Pred. No. 1.6e+02; Matches 7; Conservative 1; Mismatches 6; Indels
; REFERENCE/DOCKET NUMBER: DX0335K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-82-9196
; TELEPHONE: 415-82-9196
; TELEPHONE: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 578 amino acids
; TYPE: amino acid
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-110-683-2
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Gaps ; 0

Search completed: November 8, 2002, 19:29:22 Job time: 22.6993 secs

109 LRTEHXVXXLPDXH 122 

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Sequence 2, Application US/08110683

Septence 1, Application US/08110683

Septence 2, Application US/08110683

APPLICANT: How Alice Suk-Yue APPLICANT: How Di-Hwei APPLICANT: How Di-Hwei APPLICANT: How Di-Hwei APPLICANT: How Chuan-Chu APPLICANT: Tan, Jimmy C. APPLICANT: Chou, Chuan-Chu ITLE OF INVENTION: (IL-10)

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STREET: Qalifornia
COUWTRY: USA

ZIP: 94304-1104

COMPUTER: Floppy disk
COMPUTER: TINM FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 1; Length 578;
Pred. No. 1.6e+02;
1; Mismatches 6; Indels
                       ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,788
FILLING DATE: 19-APR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,683
FILING DATE: 23-AUG-1993
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/011,066
FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXO5/
TELECOMMUTCATION INFORMATION:
TELEPHONE: 415-852-9196
TELEPHONE: 415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.4%;
                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               : 578 amino acids amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-788-5
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Best Local Similarity
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US-08-110-683-2
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APPLICANT: Wei, Sherry
APPLICANT: Ho, Alice Suk-Yue
TITLE OF INVENTION: MAMMALIAN INTERLEUKIN-10 (IL-10)
TITLE OF INVENTION: SUPER-ACTIVATING RECEPTORS; AND VARIANTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Moore, Kevin W.
APPLICANT: Wel, Sherry
APPLICANT: Ho, Alice Suk-Yue
TITLE OF INVENTION: MAMMALIAN INTERLEUKIN-10 (IL-10)
TITLE OF INVENTION: SUPER-ACTIVATING RECEPTORS; AND VARIANTS
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 557;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

ELLING DATE:

ATTORNEY/AGENT INFORMATION:

NAME:

CLASSIFICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME:

REGISTRATION NUMBER:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE:

415.852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 1; Le
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 5, Application US/08424788

Patent No. 5716804

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 901 California Avenue
Palo Alto
                                                                                                                                                    Sequence 6, Application US/08424788 Patent No. 5716804 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERATICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.4%;
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-424-788-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 LRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 ІОТЕЕРОFLІРОРН 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
133 YLLXIWXP 140
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976 YLLSLWPP 983
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                                                                                                          RESULT 13
US-08-424-788-6
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                                                                                                                                                                                                                                                                                                                                                         Length 1876;
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Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 4; Length 187
Pred. No. 3.3e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/170,996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                        2307K-063700US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/609,049
FILING DATE: 29-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/09170996 Patent No. 6291220
FILING DATE: 29-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-240
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Molz, Lisa
APPLICANT: Chen, Yen-Wen
TITLE OF INVENTION: No. 6291220
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
                                                                                                                                               TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 amino acids
                                                                                                                                                                                                                                                                                                                                                           5.68;
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 62...
5, Conservative
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                                                                                                                                                                                                                                                        single
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MOLECULE TYPE: protein

US-09-170-996-12
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California
                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
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Best Local Similarity
Matches 5; Conserv
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US-09-170-996-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-170-996-28
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                MOLY, Lisa
Chen, Yen-Wen
Chen, Yen-Wen
WENTION: No. 5948664el PI 3-Kinase Polypeptides
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APPLICANT: Williams, Lewis T.
APPLICANT: Williams, Lewis T.
APPLICANT: Mol2, Lisa
APPLICANT: Chen, Yen-Wen
TITLE OF INVENTION: No. 6291220el PI 3-Kinase Polypeptides
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STREE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1876;
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Pred. No. 3.3e+02;
---Abas 2; Indels
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,049A
FILING DATE: 29-FEB 1996
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: DOW, KATON B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 23,07K-063700US
TELEPAMINICATION INFORMATION:
TELEPAMINICATION INFORMATION:
TELEPAMINICATION SEQUENCE: 415-326-240
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/170,996
                                                      TITLE OF INVENTION: NO. 5948664el PI 3-Kinase NUMBER OF INVENTION: NO. 5948664el PI 3-Kinase NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LI STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/609,049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/09170996
Patent No. 6291220
        Williams, Lewis T.
                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 62.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-609-049A-28
                                                                                                                                                                                                                             ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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ZIP: 94111-3834
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US-09-170-996-12
        APPLICANT:
                                                APPLICANT:
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APPLICANT: Williams, Lewis T.
APPLICANT: Wolz, Lisa
APPLICANT: Chen, Yen-Wen
TITLE OF INTERPRICES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                               Length 1839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1876;
                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE PATENTIN F. 25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,049A
FILING DATE: 29-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DOW, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-063700US
                                                                                                                                                                 Score 33; DB 2; Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 2;
Pred. No. 3.3e+02;
1; Mismatches 2
                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111.3834
COMPUTER READABLE FORM:
COMPUTER TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-08-609-049A-12
Sequence 12, Application US/08609049A;
Patent No. 5948664
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28, Application US/08609049A; Patent No. 5948664; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 230
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.68;
62.58;
                                                                                                                                                                   5.68;
                                                                                                                                                             Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                        ; FEATURE: -
; OTHER INFORMATION: 929491
US-09-172-977-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Embarcac
CITY: San Francisco
STATE: California
                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                               1493 DOSOYLLKIW 1502
                                                                                                                                                                                                                                          129 DXXXYLLXIW 138
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US-08-609-049A-28
SEQ ID NO 4
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                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: HABUCHI, OSAMI
APPLICANT: FUKUTA, MASAKAZU
TITLE OF INVENTION: POLYPEPTIDE OF GLYCOSAMINOGLYCAN
TITLE OF INVENTION: SULPOTRANSFRASE ORIGINATING FROM HUMAN AND DNA CODING
TITLE OF INVENTION: FOR THE POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                 E: KNOBBE, MARTENS, OLSON & BEAR, LLP
620 NEWPORT CENTER DRIVE, SIXTEENTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN ANKYRIN FAMILY PROTEIN
FILE REFERENCE: PP-0615 US
CURRENT APPLICATION UNMBER: US/09/172,977
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.6%; Score 33; DB 2; 45.5%; Pred. No. 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,514
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALLISE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN
                                                                                                                            Sequence 2, Application US/08899514
Patent No. 5910581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09172977 Patent No. 5989863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: DANIEL E ALTMAN
REGISTRATION NUMBER: 34,115
REFERENCE/COCKET NUMBER: TOY.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714 760 9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34,115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 714 760 9502 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-899-514-2
                                                                                                                                                                                                                                                                                                                                                      CITY: NEWPORT BEACH
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
5; Conserva
             60 DTNRYLADVWVP 71
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204 EHFITPLPEDH 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-172-977-4
                                                                                                        US-08-899-514-2
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Gaps

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ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
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                                                                                                                                                                                                                                                                                                                                                                                                                        41 DTNRYLADVWVP 52
                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                       STRANDEDNESS: S1
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-071-035-74
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Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gill H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
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                                                                              Gaps
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                                                                                                                                                                                                                                    Sequence 22, Application US/09370700

Patent No. 6274350

GENERAL INFORMATION:
APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Treadway, Patt J
APPLICANT: Turner, Jan R
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIV;
CURRENT FILING DATE: 1999-08-09
CURRENT FILING DATE: 1999-03-09
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 278
                                                                              .;
0
                                   Score 34; DB 4; Length 278;
Pred. No. 29;
0; Mismatches 7; Indels
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ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOGTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-22
                                     5.8%;
                                   Query Match
Best Local Similarity 50.0
Matches 7; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
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159 LNTEQOVAILPTSH 172
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: CLASSIFICATION:
US-09-036-987A-22
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US-709-071-035-76
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US-09-370-700-22
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: G11 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 4;
Pred. No. 20;
1; Mismatches
                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                 Score 33; DB 4
Pred. No. 17;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
                                                   PB369P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 74, Application US/09071035; Patent No. 6448043
                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
Anders Brookes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 74
                                                                                                                                                                                                                                                                                               Query Match 5.6%;
Best Local Similarity 41.7%;
Matches 5; Conservative
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                           REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                       single
                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-09-071-035-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TELEFAX: (317)337-4847
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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TITLE: Isolation and characterization of an
TITLE: extrachromosomal element from No. 6015705ardia mediterranei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBLICATION INFORMATION:
AUTHORS: G.J.W. Euverink, D.J. Wolters, L.
AUTHORS: Dijkhuizen
TITLE: Prephenate dehydratase of the actinomycete
TITLE: Amycolatopsis methanolica: purification and
TITLE: characterization of the wild-type and deregulated mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBLICATION INFORMATION:
AUTHORS: G.J.W. Euverink, G.I. Hessels, J.W.
AUTHORS: Vrijbloed, J.R. Coggins, L. Dijkhuizen
TITLE: Purlication and characterization of a dual
TITLE: function 3-hydroquinate dehydratase from Amycolatopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified amino acid, formylmethionine LOCATION: The first amino acid in the sequence, LOCATION: described as methionine, is actually known as LOCATION: formylmethionine ("fMet"). Polypeptide chains in LOCATION: bacteria often start with formylmethionine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS: L. de Boer, W. Harder, L. Dijkhuizen
TITLE: Phenylalanine and tyrosine metabolism in the
TITLE: facultative methylotroph No. 6015705ardia sp. 239
JOURNAL: Arch. Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS: J. Cairns, J. Overbaugh, S. Miller
ZIP: 60609-2828
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette
COMPUTER: Compaq Prolinea 5100
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 60/001,381
FILING DATE: 24-JUL-96
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/001,381
FILING DATE: 24-JUL-95
ATTORNEY/AGENT INFORMATION:
NAME: Daniel J. Hulseberg
REGISTRATION NUMBER: 36,554
REFERRENCE/DOCKET NUMBER: 96303755
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (312) 701-8606
TELEFAX: (312) 701-711
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: The first amil
LOCATION: described as I
LOCATION: formylmethion
LOCATION: bacteria often
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 192 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE:
JOURNAL: J.
VOLUME: 138
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DATE: 1988
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DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE: en
JOURNAL:
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JOURNAL:
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                                                             PUBLICATION INFORMATION:
AUTHORS: J. Sambrock, E.F. Frisch, T. Maniatis
AUTHORS: J. Sambrock, E.F. Frisch, T. Maniatis
TITLE: Molecular cloning: a laboratory manual
JOURNAL: Cold Spring Harbor Laboratory Press
DATE: 1989
PUBLICATION INFORMATION:
AUTHORS: J.W. VIIDLOGG, J. Madon, L. Dijkhuizen
TITLE: a plasmid from the methylotrophic
TITLE: actinomycetce Amycolatopsis methanolica capable of site-
TITLE: Specific integration
JOURNAL: J. Bacteriol.
VOLUME: 176
PAGES: 7087-7090
DATE: 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Merlo, Donald J.
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway Patti J.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.8%; Score 34; DB 3; Length 192; Best Local Similarity 24.1%; Pred. No. 20; Matches 7; Conservative 3; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 RTEHXVXXLPDXHXXLXXXDXXXYLLXIW 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 REEHHTVWFPPVAMAIVFNDTADHVLMAW 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/036,987A FILING DATE: 09-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22, Application US/09036987A Patent No. 6143526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Dow AgroSciences I
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
VOLUME: 14
PAGES: 126-133
DATE: 1985
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linear

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RESULT 2
US-08-685-466C-4
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Seguence 74,
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US-08-884-072-6
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US-09-035-466C-4
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US-09-071-035-76
US-09-071-035-74
US-08-609-049A-12
US-09-172-977-4
US-09-172-977-4
US-09-170-996-12
US-09-170-996-12
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US-08-424-788-5
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US-09-199-637A-215
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 GenCore version
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Listing first 45 summaries
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Sequence 15, Application US/09376330

Sequence 15, Application US/09376330

Sequence 15, Application US/09376330

GENERAL INFORMATION:
APPLICANT: Tessier. Daniel C.
APPLICANT: Dignard, Daniel C.
APPLICANT: Dignard, John J.M.
APPLICANT: Dignard, John J.M.
TITLE OF INVENTION: Method for Screening for TITLE OF INVENTION: and nucleic acid encoding for UGGT
TITLE OF INVENTION: and nucleic acid encoding for UGGT
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Patent No. 6015705
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Method of Modifying the DNA of an TITLE OF INVENTION: Organism, DNA Sequence, Method of Detection and TITLE OF INVENTION: Isolation of a Gene Capable of Modifying the DNA TITLE OF INVENTION: Organism and Organisms Comprising Modified DNA NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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28.2%; Pred. No. 5.1;
US-09-212-168-6

US-09-071-035-404

US-09-071-035-402

US-08-414-926A-8

US-08-926-922-8

US-09-253-657-8

US-09-247-373B-20

US-09-247-373B-20

US-09-247-373B-20

US-09-247-373B-20

US-09-247-373B-20

US-09-134-001C-4141

US-08-973-005A-12

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STREET: P.O. Box 2828
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Matches 11; Conservative
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R APPLICATION NUMBER: 60/082797
R FILING DATE: 1998-04-22
R FILING DATE: 1998-04-28
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R FILING DATE: 1998-04-28
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083495
R APPLICATION NUMBER: 60/083496
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R APPLICATION NUMBER: 60/085700
R FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/086023
R FILING DATE: 1998-05-18
R APPLICATION NUMBER: 60/086392
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APPLICATION UNMBER: 60/085573
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
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APPLICATION NUMBER: 60/082569
FILING DATE: 1998-04-21
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APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/084114
FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084639
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APPLICATION UNMBER: 60/084640
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APPLICATION NUMBER: 60/084643
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APPLICATION UNMBER: 60/086486
FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/087098
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FILING DATE: 1998-05-28
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APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
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APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/081838
                                    APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/085582
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/088217
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APPLICATION NUMBER:
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R APPLICATION NUMBER: 60/088863 R FILING DATE: 1998-06-11 R PLILING DATE: 1998-06-11 R PLILING DATE: 1998-06-11 R APPLICATION NUMBER: 60/089090 R FILING DATE: 1998-06-12 R APPLICATION NUMBER: 60/089105 R FILING DATE: 1998-06-12 R APPLICATION NUMBER: 60/088655
R FILING DATE: 1998-06-09
R APPLICATION NUMBER: 60/088722
RR FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088738
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088740 R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088811
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08824
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08825
R FILING DATE: 1998-06-10 1998-06-05 UUMBER: 60/088326 APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089514 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-66-10 APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 PRIOR APPLICATION NUMBER: 60/089598 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089553 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17 1998-06-04

8, 2002, 19:29:44 Search completed: November Job time: 12.0654 secs

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Query Match 5.3%; Score 31; DB 12; Length 1894; Best Local Similarity 19.0%; Pred. No. 3.2e+02; Matches 4; Conservative 0; Mismatches 17; Indels

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITTLE OF INVENTION: ACIDS ENCODING THE SAME
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APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08
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Fatent No. US2020066288A1
GENERAL INFORMATION:
APPLICANT: Lodgs, Michael J.
APPLICANT: Wang, Tongtong
APPLICANT: Gerrist, Heather
APPLICANT: Mohamath, Raodoh
APPLICANT: Indirias, Carol Y.
APPLICANT: Farm, Ligun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SEQ ID NO 429
ENOTHER OF SECOND OF MINDOWS VERSION 4.0
SED ID NO 429
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Pred. No.
                                                                                                                                                                                                                        CLONE: 496120
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
TELEPHONE: 415-855-0555
TELEFAT. 415-845-4166
TELEX: TELEX: TELEX: CURKNOWN>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHRACTERIZICS:
LENGTH: 559 amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                     Query Match 5.3%;
Best Local Similarity 50.0%;
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Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
                                                                                                                                                                                                       LIBRARY: GenBank
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                                                                                                                                                                                                                                                                                                                                             6; Conservative
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Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                   109 LRTEHXVXXLPD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 LRTEHXVXXLPD 120
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59 LRVDHSVTSLHD 70
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US-09-833-790-429
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31; DB 10; Length 559;
Pred. No. 92;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ_for Windows Version 2.0
                                                                                                                                                                                                                                                             TITLE OF INVENTION: Human Extracellular Matrix-1
FILLE REFERENCE: PF223C1
CURRENT APPLICATION NUMBER: US/09/854,549
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 09/007,105
PRIOR PPLICATION NUMBER: US 60/035,711
PRIOR FILING DATE: 1998-01-14
PRIOR FILING DATE: 1997-01-16
PRIOR FILING DATE: 1997-01-16
PRIOR FILING DATE: 1997-01-16
PRIOR FILING DATE: 1997-01-16
PRIOR SEQ ID NOS: 9
NUMBER OF SEQ ID NOS: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0333 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/836,561
FILING DATE: 16-Apr-2001
CLASSIFICATION: <UNIVERSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/212,168
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                                                                                                                                                                                                  Sequence 7, Application US/09854549 Patent No. US20010034334A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09836561; Patent No. US20020038006A1; GENERAL INFORMATION:
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Corley, Neil C.
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Best Local Similarity 50.0%;
Matches 6; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
                               109 LRTEHXVXXLPD 120
                                                               353 IKSHHNVGGLPD 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mus musculus
US-09-854-549-7
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59 LRVDHSVTSLHD 70
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US-09-836-561-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 513;
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Anamoto, Robert T.
APPLICANT: An H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
84;
                                         FRICK FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FASTSEQ for Windows Version 4.0

SCOTUD NO 12406
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10987
LENGTH: 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31;
Pred. No.
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CURRENT APPLICATION NUMBER: US/09/815,242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10987, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
FILING DATE: 2000-03-21 APPLICATION NUMBER: 60/206,848
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                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12406
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Best Local Similarity 29.4%;
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserva
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US-09-815-242-10987
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104 KXXXXLRTEHXVXXLPD 120
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APPLICANT:
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## APPLICANT: Schaffner, Gotthold
### TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
### FILE REPERENCE: 0652.1800001
### CURRENT APPLICATION UNBER: US/09/970,711
### CURRENT FILING DATE: 2001-10-05
### PRIOR FILING DATE: 1999-01-12
### PRIOR FILING DATE: 1997-04-18
### PRIOR FILING DATE: 1997-04-18
### PRIOR FILING DATE: 1997-04-18
### SOFTWARE: PatentIn Ver. 2.0
### SOFTWARE: PatentIn Ver. 2.0
### ILINGTH: 206
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APPLICANT: 2yskind, Judith W.
APPLICANT: 42yskind, Judith W.
APPLICANT: 42yskind, Judith W.
APPLICANT: 42yskind, Judith W.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential
FILE REFERENCE: ELITRA.011A
TITLE OF INVENTION: PROKARYORES
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/2011,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 10; Length 206;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5490
LENGTH: 506
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Patent No. US20020061569A1
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Zyskind, Judith W.
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APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.3
Best Local Similarity 42.9
Matches 6; Conservative
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Best Local Similarity 29.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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Pred. No. 83;
                                                                                                                                                                                                                                                                                                                      APPLICANT: Trans. Mail.

APPLICANT: Trans. John D.

APPLICANT: Trans. John D.

APPLICANT: Carr, Grant J.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes

CURRENT APPLICATION NUMBER: 05/191,078

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/259,308

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/259,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SSOFTWARE: ESSESEQ for Windows Version 4.0
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APPLICANT: Carr, Grant J.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION:
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12406, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                            Sequence 11555, Application US/09815242 Patent No. US20020061569A1
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PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Helicobacter pylori
US-09-815-242-11555
                                                                                                                                                                                                                                                       Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
331 KTAQTIKSHHNVGGLPE 347
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Best Local Similarity 41.7
Matches 5; Conservative
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                                                                                             RESULT 9
US-09-815-242-11555
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HIT: BE300193.1, EVALUE 4.00e-08
HIT: Q49412, EVALUE 4.70e+00
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N: EXPRESSED IN BT474, SIGNAL = 73

N: EXPRESSED IN FETAL LIVER, SIGNAL = 28

N: EXPRESSED IN HELALO, SIGNAL = 19

N: EXPRESSED IN HEART, SIGNAL = 14

N: EXPRESSED IN LONG, SIGNAL = 14

N: EXPRESSED IN BRAIN, SIGNAL = 59

N: EXPRESSED IN PLACENTA, SIGNAL = 7.3

N: EXPRESSED IN PLACENTA, SIGNAL = 56

N: EXPRESSED IN PLACENTA, SIGNAL = 56

N: EXPRESSED IN BONE MARROW, SIGNAL = 30

N: EXPRESSED IN BONE MARROW, SIGNAL = 30
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Pred. No. 6.2;
PRIOR FILLING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILLING DATE: 2000-09-27
PRIOR PRILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR FILLING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-20
SOUTHWARE ADDIOR ADDI
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; Sequence 13, Application US/09970711
; Patent No. US20020081279A1
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Chlocca, Susanna
Kurzbauer, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 35.7
Matches 5; Conservative
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: BOTHER INFORMATION: BOTHER INFORMATION: EOTHER INFORMATION:
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Patent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HOMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
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EXPRESSED IN BRAIN, SIGNAL = 1.2
EXPRESSED IN BONE MARROW, SIGNAL = 1.1
EXPRESSED IN ADDLT LIVER, SIGNAL = 0.9
EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
EST_HUMAN HIT: BF529379.1, EVALUE 3.00e-03
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                                                                   PRIOR APPLICATION NUMBER: GB 2423.5
PRIOR APPLICATION NUMBER: GB 2423.5
PRIOR APPLICATION NUMBER: GB 60/236,359
PRIOR APPLICATION NUMBER: DCT/USO1/00666
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PLING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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Matches 6; Conservative
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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US-09-864-761-34686
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Sequence 42872, Application US/09864761

Patent No. US2002004876341

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456
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Patent No. US20020048795A1
GENERAL INFORMATION:
APPLICANT: FARMICK, Mike
TITLE OF INVENTION:
FILE REFERENCE: 032301 WD 212
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CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.98

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.96

CTHER INFORMATION: EST_HUMAN HIT: BE278123.1, EVALUE 1.00e-20

US-09-864-761-46893
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PELLING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 46893
LENGTH: 54
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Pred. No. 5.1;
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CURRENT FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
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PRIOR APPLICATION NUMBER: US 09/632,366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 HVVATMPDLYHLLVELNAVQSLLGL 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.0%
Matches 7; Conservative
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US-09-864-761-42872
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                                                                                                                                                                                                                                                                                TYPE: PRT
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE PERENCE: According to The Color of Colo
                         APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 311338
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/761,142
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR PILING DATE: 2000-01-14
NUMBER OF SED ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 46893, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 DXHXXLXXXDXXXYLLXIWXP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 DGHFALTTRDNSIYLVIVHLP 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 33.3
Matches 7; Conservative
      Bachmann, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-864-761-46893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-108-605-237
                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 237
LENGTH: 3503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
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Sequence 237, App
Sequence 237, Appl
Sequence 4689, A
Sequence 4287, A
Sequence 3468, A
Sequence 1155, A
Sequence 1155, A
Sequence 1155, A
Sequence 1206, A
Sequence 7, Appl
Sequence 7, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 16, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 121, App
                                                                                                         8, 2002, 19:26:04; Search time 9.06536 Seconds (without alignments) 464.428 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gnz_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-946-143-2
US-09-946-143-2
US-09-946-143-8
US-09-970-711-13
US-09-970-711-13
US-09-815-242-1406
US-09-815-242-110987
US-09-815-242-10987
US-09-815-242-10987
US-09-815-242-10987
US-09-813-561-6
US-09-83-561-6
US-09-83-561-6
US-09-933-777-16
US-09-903-456-41
US-09-903-456-41
US-09-903-456-41
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                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                        92612 seqs, 14418503 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA:*
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Maximum Match 1008
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
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Match Length DB
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70	30	2 · T	199	0 T	US-09-864-/61-33661	
21	30	5.1	209	10	US-09-764-864-800	Sequence 800, App
22	30	5.1	210	10	US-09-811-284-229	Sequence 229, App
23	30	5.1	214	12	US-10-078-929-66	99
24	30		234	10	US-09-912-020-350	
25	30	5.1	273	10	US-09-216-393-12	12,
26	30		283	10	US-09-903-456-85	
27	30	5.1	292	10	US-09-764-864-1261	
28	30		292	10	US-09-903-456-65	65,
29	30	5.1	423	10	US-09-925-300-1233	Sequence 1233, Ap
30	30	5.1	502	10	US-09-323-998D-56	Seguence 56, Appl
31	30	5.1	1422	8	US-08-424-550B-81	Sequence 81, Appl
32	30	5.1	1497	10	0 US-09-060-854B-2	Sequence 2, Appli
33	30	5.1	4440	12	US-10-052-586-525	Sequence 525, App
34	30	5.1	4679	10	US-09-804-898-2	Sequence 2, Appli
35	9	5.0	272	10	US-09-925-118-2	7
36	29.5	5.0	1386	10	US-09-866-582-38	ñ
37	29	4.9	16	10	US-09-822-698A-51	S
38	29	4.9	44	10	US-09-864-761-37419	3743
39	29	4.9	9	σ	US-10-046-961-17	
40	29	4.9	70	10	US-09-864-761-49072	(1)
41	29	6.4	80	10	US-09-894-018-97	
4.2	29	6.4	86	10	US-09-894-018-101	101,
43	29	4.9	106	10	US-09-894-018-95	95.
44	29	6	107	2	-894	93.
45	52	6.4	107	10	894-018-1	
					ALIGNMENTS	
L E III						
US-09-764-855-121	4-855-12	Ţ				

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: LOCATION: (231)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-855-121
                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
COGATION: (152)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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0
                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PAll0
CURRENT APPLICATION NUMBER: US/09/764,855
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 334
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 121
LENGTH: 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 10; Length 233;
Pred. No. 1.8;
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Sequence 237, Application US/10108605
Patent No. US20020160934A1
GENERAL INFORMATION:
APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
Sequence 121, Application US/09764855
Patent No. US20020119919A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 RTEHXVXXLPDXH 122
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                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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RESULT 15
F81423
L-lactate permease Cj0076c [imported] - Campylobacter jejuni (strain NCTC 11168)
C; Species: Campylobacter jejuni
C; Species: Campylobacter jejuni
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C; Accession: F81423
R; Parkhill, J; Wren, B.W; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A; Accession: F81423
A; Coloure type: DNA
A; Residues: 1-560 - PAR>
A; Cross-references: GB:AL139074; GB:AL111168; NID:66967505; PIDN:CAB72562.1; PID:g696757
A; Experimental source: serotype O2, strain NCTC 11168
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Coloured to the permease
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                                       Gaps
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                                       18; Indels
Best Local Similarity 26.7%; Pred. No. 26;
Matches 8; Conservative 4; Mismatches
                                                                                                       111 TEHXVXXLPDXHXXLXXXDXXXYLLXIWXP 140
                                                                                                                                                                       260 TOGOMVNVNDSLVQLTPSDNPYYCLVLWVP 289
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Qy Dp Search completed: November 8, 2002, 19:26:48 Job time: 24.085 secs

9 13:04:27 2002

Sat Nov

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Gaps

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Indels

Length 1066;

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C; Accession: D69786
R; Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M; Alloni, G; Azevedo, V; Ber C; Bron, S; Brouillet, S; Bruschi, C.V; Caldwall, B; Capuano, V; Carter, N.M; A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C; Ferrari, Nature 390, 249-256, 1997
A; Authors: Foulger, D; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A; Galicch, J; Harwood, C.R.; Henaut, A.; Hilbert, H; Holsappel, S; Hosono, S; Hullo, M Koetter, P; Koningstein, G; Krogh, S; Kumano, M; Kurita, R.; Lapidus, A; Lardino, A; Authors: Lauber, J; Lazarevic, V; Lee, S.M; Levine, A; Liu, H; Masuda, S; Mau Y, M; Ogawa, K; Ogiwara, A; Oudega, B; Park, S.H; Parro, V; Pohl, T.M; Portete Rieger, M; Rivolta, C; Rocha, B; Roche, B; Rose, M; Sadie, Y; Sato, T; Scanla, Authors: Schleich, S; Schroeter, R; Scoffone, F; Sakiguchi, J; Sekowska, A; Se akeuchi, M; Tamakoshi, A; Tanaka, T; Terpstra, P; Tognoni, A; Tosato, V; Uchiya T; Winters, P; Wipat, A; Yamaneto, H; Yamane, K; Yasamoto, K; Yata, K; Yata, K; Yoshida A; Authors: Voshikawa, H; Danchin, A; Tosato, V; Uchiya A; Title: The complete genome sequence of the Gram-Positive bacterium Bacillus subtili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: ABB013
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G il, M.; Ruhberford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Accession: D69786
A.Status: preliminary: nucleic acid sequence not shown; translation not shown A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-229 <a href="https://doi.org/10.10/">KCMNA
A.Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12411.1; PID:g26329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB: AL590842; PIDN: CAC88964.1; PID: 915978208; GSPDB: GN00175 C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycoprotein endopeptidase homolog ydic - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
F;156-172/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                     Score 36; DB 2;
Pred. No. 37;
3; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain 168
C; Genetics:
A; Gene: ydiC
C; Superfamily: hypothetical protein HI0388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 LRTEHXVXXLPDXHXXLXXXD 129
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33.38;
                                                                         6.1%;
|larity 35.7%;
|Conservative
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Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-411 <KUR>
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Nilternate names; protein NOTS; protein YNL267w

C.Species: Saccharowyces cerevisiae

C.Species: Saccharowyces

R.Scharows Saccharowyces

R.Scharows Saccharowyces

R.Scharows Saccharowyces

R.Scharows Saccharows

A.Scharows Saccharows

A.Scharows

A.Scharows Saccharows

A.Scharows

A.
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A; Residues: 1-106 (SEW)
A; Cross-references: BMBL:271543; NID:g1302325; PIDN:CAA96174.1; PID:e239719; PID:g130232
A; Experimental source: strain $288C
A; Experimental source: strain $288C
B; Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.
Yeast 12, 505-514, 1996
A; Title: The sequence of a 24 152 bp segment from the left arm of chromosome XIV from Sa
A; Reference number: $65111; MUID:96310631; PMID:8740425
                        A;Cross-references: GB:AE004723; GB:AE004091; NID:g9949067; PIDN:AAG06364.1; GSPDB:GN001ASperimental source: strain PAO1A;Genetics: PA2976A;Genetics: PA2976C; PA2976C; Superfamily: ribonuclease E
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                                                                                                                                                                                                                                                                      Length 1057;
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A;Map position: 14L
C:Keywords: nucleus; phosphotransferase; transmembrane protein
                                                                                                                                                                                                                                                                      Score 36; DB 2;
Pred. No. 36;
1; Mismatches
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A;Molecule type: DNA
A;Residues: 721-960 <SEF>
                                                                                                                                                                                                                                                                          6.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: SGD: PIK1; PIK41; PIK120
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A; Residues: 1-1066 <SEN>
A; Residues: 1-1057 <STO>
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Matches 7; Conserv
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Gaps

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12;

Length 229, Indels

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DB 2; Length 411;
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999 C;Accession: B69305
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Best Local Similarity 50...
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Matches 7; Conserv
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A;Molecule type: DNA
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H83273
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                                                                                                                                                                                                               RESULT 7
T4374
dynein heavy chain, cytosolic - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T43274
R;Yamamoto, A.; West, R.R.; McIntosh, J.R.; Hiraoka, Y.
J. Cell Biol. 145, 1233-1250, 1999
A;Title: A cytoplasmic dynein heavy chain Is required for oscillatory nuclear movem A;Reference number: 222383; MulD:99296615; PMID:1036596
A;Accession: T43274
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-4196 <YAM>A;Residues: 1-4196 <YAM>A;Residues: 1-4196 <YAM>A;Residues: BMBL:AB006784; NID:92351080; PIDN:BAA22056.1; PID:92351081
A;Experimental source: strain_CRLi52
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Geneticn: 1
C;Superfamily: dynein heavy chain, cytosolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein W04D2.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Cat-1999 #sequence_revision 15-oct-1999 #text_change 15-oct-1999
C;Accession: T26148
R;Lennard, N.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z20161
A;Accession: T26148
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Olecule type: DNA
A;Residues: 1-624 <WIL>A;Residues: 1-624 <WIL>A;Coss-references: EMBL:Z75552; PIDN:CAA99942.1; GSPDB:GN00023; CESP:W04D2.4
A;Residues: 1-624 <WIL>A;Coss-references: EMBL:Z75552; PIDN:CAA99942.1; GSPDB:GN00023; CESP:W04D2.4
A;Experimental source: clone W04D2
C;Genetics:
A;Gene: CESP:W04D2.4
A;Map position: 5
A;Introns: 23/3; 112/3; 183/2; 402/2; 495/1; 523/3
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                                                                   Gaps
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           DB 2; Length 1540;
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                                                                 13; Indels
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                                                                 1; Mismatches
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2; Mismatches
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                    Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38;
                                                                                                                                             990 DHDVSTLHDLHNALRGVDNVLY 1011
                                                                                                           112 EHXVXXLPDXHXXLXXXDXXXY 133
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Best Local Similarity 36.8%;
Matches 7; Conservative 2
                    6.4%;
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                Query Match
Best Local Similarity 36.43
Matches 8; Conservative
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Best Local Similarity 64.3
Matches 9; Conservative
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R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod S:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A.Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A.Tille: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A; Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G. Species: Salmonella enterica subsp. enterica serovar Typhi
A.Note: this species has also been called Salmonella typhi
A.Note: this species has also been called Salmonella typhi
G. Baccession: AH0853
B. Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronhi, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
S.; Moule, S.; O'Gacra, P.
Nature 413, 848-852, 2001
A.Athors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A.Reference number: AB0502; PMID:1167608
A.Reference number: Salmonella enterica se
A.Retaus: preliminary
A.Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-239 <KLE> A;Residues: 1-239 <KLE> A;Cross-references: GB:AE001074; GB:AE000782; NID:g2689397; PIDN:AAB90792.1; PID:g265 C;Superfamily: conserved hypothetical protein H11191
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A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83273
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A.; Larbig,
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A;Cross-references: GB:AL513382; PIDN:CAD06015.1; PID:g16503984; GSPDB:GN00176
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9.7;
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15.0%; Pred. No. 30;
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Pred. No. 9.7;
0; Mismatches
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990 DHDVSTLHDLHNALRGVDNVLY 1011
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Matches 11; Conserv
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Matches 8; Conserv
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C; Date: 23-Aug-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C; Accession: S54724
EMBO J. 14, 1294-1303, 1995
A; Title: Drosophila UDP-glucose: Jyen glucosyltransferase: sequence and character A; Reference number: S54723; MUID:95246722; PMID:7729408
A; Accession: S54723
A; Mulecule type: mRNA
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-1548 CPAR>
A; Cross-references: GB:U20554; NID:9790584; PIDN:AAA85850.1; PID:9790585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 4
A;Introns: 41/3; 70/3; 88/1; 118/1; 321/1; 367/1; 474/1; 504/2; 624/3; 655/2; 667/3; 695
A;Note: F28A23.180
C;Superfamily: Arabidopsis thaliana hypothetical protein F28A23.180
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R;Bevan, M.; Weichselgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, is submitted to the Protein Sequence Database, October 1998
A;Reference number: 215415
A;Accession: T05430
A;Molecule type: DNA
A;Residues: 1-917 **SBEV}
A;Residues: 1-917 **SBEV}
A;Eross-references: EMBL:AL021961
A;Eross-references: EMBL:AL021961
A;Eross-references: Cultivar Columbia; BAC clone F28A23
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: D84781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                    ω
•
                                                                                                   A;Molecule type: DNA
A;Residues: 1-1207 <STO>
A;Cross-references: GB:AE002093; NID:g4581149; PIDN:AAD24633.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g36490
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F28A23.180 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1094 KNISQLRTEHRVYELPDEHPLLAQLEKREPDDPCSYLLAIWTP-GETADSIQPSVSTC-- 1150
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                          Length 1207;
                                                                                                                                                                                                                                                                                                                                              56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 77; DB 2; Length 917;
Pred. No. 2.4e-08;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 KXXXXLRTEHXVXXLPDXHXXL-----XXXXDXXXYLLXIWXP 140
                                                                                                                                                                                                                                                                                       15.4%; Score 91; DB 2; ]
29.8%; Pred. No. 2.3e-11;
Live 0; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1151 -IFQANGMLCDEETCFSCNSIKETRSQIVRGTIL 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.1%; Score 77; DB 3
Best Local Similarity 44.2%; Pred. No. 2.4e-
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 29.89
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: S54724
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-37 <PA2>
                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Conetics:
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C. Species: Mycobacterium leprae
C. Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-May-2001
C. Species: Mycobacterium leprae
C. Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-May-2001
C. Accossion: H87203
R. Cole, S.T.; Eiglimeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holro eam, M.A.; Rutherford, K.M.
Alautre 409, 1007-1011, 2001
A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; A.Title: Massive gene decay in the leprosy bacillus.
A.Accession: H87203
A. Secsion: H87203
A. Status: preliminary
A. Molecule type: DNA
A. Molecu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: pksC
C;Superfamily: Streptomyces hygroscopicus probable polyketide synthase module 4; 3-ox
homology; [acyl-carrier-protein] S-malonyltransferase homology
C;Keywords: carrier protein
F;54-455/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OASI>
F;553-840/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;1155-1334/Domain: short-chain alcohol dehydrogenase homology <SADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: ML2356
C;Superfamily: Streptomyces hygroscopicus probable polyketide synthase module 4; 3-ox
homology; [acyl-carrier-protein] S-malonyltransferase homology
C;Reywords: carrier protein
                                                                                                                                                                                                                                            experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyketide synthase pksC - Mycobacterium leprae
Nalternate names: L518_F1_2 protein
C; Species: Mycobacterium leprae
C; Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C; Accession: S73013
R; Smith, D.R; Robison, K.
submitted to the EMBL Data Library, November 1993
A; Description: Mycobacterium leprae cosmid L518.
A; Reference number: S72591
A; Reference number: S72591
A; Recession: S73013
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1446 <SMI>A; Coss-references: EMBL:U00023; NID:9467194; PIDN:AAA17356.1; PID:9467199
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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A;Gene: FlyBase:Ugt
A;Cross-references: FlyBase:FBgn0014075
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
C;Keywords: alycoprotein; glycosyltransferase; hexosyltransferase
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-1548/Product: UDP-glucose-dlycoprotein glucosyltransferase #status expk
F;181,266,864/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                       6.9%; Score 41; DB 2; Length 1548;
llarity 28.2%; Pred. No. 3.9;
Conservative 2; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.4%; Score 38; DB 2; Length 1446; 36.4%; Pred. No. 17; tive 1; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyketide synthase [imported] - Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 PXXXXXXXXXXXXLRTEHXVXXLPDXHXXLXXXXXXXYL 134
```

5.1.3 Compugen Ltd version - 2002 GenCore Copyright (c) 1993

sw model protein search, using OM protein 8, 2002, 19:24:14; Search time 19.085 Seconds (without alignments) 1470.857 Million cell updates/sec November Run on:

US-09-840-743-73 590 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB R Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		hypothetical prote	_		ь-	polyketide synthas		->	hypothetical prote	ä	DNA mismatch repai	ribonuclease E PA2	1-phosphatidylinos	glycoprotein endop	probable exported	L-lactate permease	al		probable thioredox	transcription requ	hypothetical prote		transcription requ	probable UDP-N-ace	monooxygenase homo	GMP synthase (glut	Putative L-lactate	L-lactate permease	probable L-lactate	formate dehydrogen
SUMMARIES		T48454	D84781	T05430	S54723	S73013	н87203	T43274	T26148	B69305	AH0853	н83273	A49335	D69786	AB0013	F81423	H90451	T10358	B72454	D87450	H81213	B81790	A87451	D71331	F69833	E70321	E65083	F83050	$^{\circ}$	AI3556
DB	!	CZ	7	~	~	N	~	~	~	7	~	~	7	7	7	7	~	7	7	7	~	~	~	~	~	~	2	~	N	7
Length 1	1	234	1207	917	1548	1446	1540	4196	624	239	855	1057	1066	229	411	260	762	249	250	298	322	322	332	459	499	510	260	562	267	786
% Query Match		24.7	Š.	13.1	6.9	6.4	6.4	6.4		6.1									5.8								5.8			5.8
Score		146	91	77	41	38	38	38	37	36	36	36	36	35	32	32	32	34	34	34	34	34	34	34	34	34	34	34	34	34
Result No.		-	7	m	. 4	Ŋ	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

general secretion hypothetical prote	hypothetical prote	halocyanın precurs probable alkyl hyd	probable peroxired	hypothetical prote	RNA polymerase alp	probable transposa	. glycosyl transfera	probable aminometh	hypothetical prote	DNA mismatch repai	thiazide-sensitive	O-antigen biosynth	phosphoinositide 3
D87271 T21490	T21486	G84236 C71065	C75081	T05450	A82715	S16891	G95205	D97532	AD2751	AD0407	A47296	T18556	T13801
7 7	77	7 (7	7	7	~	7	7	7	7	7	7	7	7
368 106	142	15/ 216	216	264	332	380	398	473	473	851	1023	1275	1876
5.7	9.1	0 W 0.0	2.6	9.0	5.6	5.6	9.9	2.6	9.6	5.6	5.6	5.6	5.6
33.5	88	33 E	33	33	33	33	33	33	33	33	33	33	33
30	32	33 34	35	36	37	38	33	40	41	42	43	44	45

## ALIGNMENTS

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A; Map position: 5
A; Introns: 49/2; 61/3; 81/1; 127/3; 149/3; 188/1; 201/1
A; Note: T32M21.180
```

10; 24.7%; Score 146; DB 2; Length 234; 26.2%; Pred. No. 3e-24; tive 0; Mismatches 134; Indels 1 Conservative Query Match Best Local Similarity Matches 51; Conserv

3; 95 -GGKASGKMCFDETCSECNSLREANSQTVRGTLLIPCRTAMRGSFPLNGTYFQVNELFAD 153 104 KXXXXLRTEHXVXXLPDXHXXLXXXDX-----XXYLLXIWXPXXXXXXXXXXXXXXXX 157 ò a òγ q

154 HESSLKPIDVPRDWIWDLPRRTVYFGTSVTSIFRGLSTEQIQFCFWKGFVCVRGFEQKTR 213 δλ g

278 XPXXLXXXLHXXXSK 292 δλ

| | | | || || || || 214 APRPLMARLHFPASK 228 Dp

RESULT 2 D84781

hypothetical protein At2936490 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001
C;Accession: D84781
R;Lin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999

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Moon D.H., Nagai M.A., Nascinento A.L.T.O., Netto L.E.S.,
Nania A. Jr., Nabrega F.G., Nunes L.R., Oliveira M.A.,
Nania A. Jr., Nabrega F.G., Nunes L.R., Oliveira M.A.,
A de Oliveira M.C., de Oliveira R.C., Palmieria D.A., Paris A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
A de Oliveira M.C., de Sar K.G., Santelli R.V., Sawasaki H.E.,
A da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
A da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
A da Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A ganoma sequence of the plant pathogen Xylella fastidiosa.";
I hature 406:151-159(2000)
I Nature 406:151-159(2000)
I OF DNA DEPENDENT RNA POLYMERASE CATAIYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and a stis content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                             (RNA)(N).
SUBINIT: CONSISTS OF A SIGMA FACTOR AND THE RNAP CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, 1 BETA' CHAIN AND 1 OWEGA CHAIN (BY SIMILARITY).
DOMAIN: THE AMINO-TERMINAL PORTION IS INVOLVED IN THE ASSEMBLY OF CORE RNAP, WHEREAS THE C-TERMINAL IS INVOLVED IN INTERACTION WITH TRANSCRIPTIONAL REGULATORS (BY SIMILARITY).
SIMILARITY: BELONGS TO THE RNA POLYMERASE ALPHA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.6%; Score 33; DB 1; Length 332; 35.7%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR01700; RNA_pol_A_bac.
Pfam: PF01000; RNA_pol_A_bac; 1.
Pfam: PF03118; RNA_pol_A_CTD; 1.
ProDom; PD001179; RNA_pol_A_bac; 1.
Transferase; Transcription; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
SEQUENCE 332 AA; 36554 MW; 98BDE535F753A577 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003951; AAF83986.1; -. HSSP; P00574; 1COO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 35./*,
                                                                                                                                                                                                                                                                                                                                                                         SUBSTRATES.
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Search completed: November 8, 2002, 19:27:16 Job time : 15.4967 secs

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Gaps

;

5; Indels

4; Mismatches

109 LRTEHXVXXLPDXH 122 ::|:| | : | | 115 IKTDHNVEIINDGH 128

δλ g œ

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NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=9a5c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPOA_XYLFA
Q9PE52;
                                                                                                                                                                                                                                                                                                        ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
RPOA_XYLFA
                                                                                                                                                                                                                                                                                                                                                                                δŏ
                                                                                                                                                                                                                                                                                                                                                                                                   g
     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                             'Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Pyrococcus.
                                                                                                                                                                                                                                                                                                                                 structure and evolution.";
structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. TDXH SUBFAMILY.
                                                                           ;;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 1; Length 216;
Pred. No. 11;
                                                      Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
COASBEES14612179 CRC64;
                                142 AA; 16075 MW; B496362F0BFEC354 CRC64;
                                                    Score 33; DB 1;
Pred. No. 7.1;
3; Mismatches
                                                                                                                                                                                      (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable peroxiredoxin.
                                                                                                                                                                     216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
TIGRFAMS; TIGR01080; rplX_A_E; 1.
PROSITE; PS01108; RIBOSOMAL_L24; 1.
Ribosomal protein.
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ248286; CAB49952.1; -. HSSP; P30041; 1PRX.
InterPro: IPR000866; AhpC-TSA.
Pfam; PF00578; AhpC-TSA; 1.
Antioxidant; Complete proteome.
ACT_SITE 46 BY SEQUENCE 216 AA; 24758 MW; CO
                                                      5.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.6%;
                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                      Probable peroxiredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus horikoshii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 LRTEHXVXXLPD 120
                                                                                             109 LRTEHXVXXLP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 VKTTHGVIKLPD 24
                                                                                                         |||:| : :|
38 LRTKHGIRAIP 48
                                                                                                                                                                                                                                                                                                       STRAIN-GE5 / Orsay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity
                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          Pyrococcus abyssi.
                                                                                                                                                                                                                                                                        NCBI_TaxID=29292;
                                                                                                                                                                                       16-OCT-2001
                                                                                                                                                                                                 16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDXH_PYRHO
058966;
                                                                                                                                                                    TDXH_PYRAB
                                                                                                                                                                                                                                                                                                                  Heilig R.;
                                 SEQUENCE
                                                      Query Match
                                                                                                                                                                               Q9UZV4;
                                                                                                                                                                                                                                PAB1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PH1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDXH_PYRHO
                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                               RESULT 13
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Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
A Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Canargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
Coutinho L.L., Cristofani M., Dias.Neto E., Docena C., El-Dorry H.,
Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
A Ganier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitalima J.P.,
A Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper B.L., Kitalima J.P.,
Lemos E.G.M., Lemos M.V.F., Lopes C.R., Machado J.R.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
A Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
                                   Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sakine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (Transcriptase alpha chain) (RNA polymerase alpha subunit).

RPOA OR XF1176.
Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                           thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
-1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. TDXH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.6%; Score 33; DB 1; Length 216; 50.0%; Pred. No. 11; 4; Indels iive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
A95DF14BF3874CA9 CRC64;
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MEDLINE=98344137; PubMed=9679194;
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InterPro; IPR000866; AhpC-TSA.
Pfam; PF00578; AhpC-TSA: 1.
Antioxidant; Complete proteome.
ACT_SITE 46 46 B)
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Matches 6; Conservative
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SEQUENCE FROM N.A.
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                                   Repeat;
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Q19869;
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SEQUENCE
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                                    yase;
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RL26_CAEEL
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                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=92000795; PubMed=1680356;
Kore-Eda S., Murayama T., Uno I.;
"Isolation and characterization of the adenylate cyclase structural
                                                                                                                                                                                                                                                                                                                                                                                                           01.JUL-1993 (Rel. 26, Created)
1-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Adenylate cyclase (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene of Neurospora crassa.";
Jpn. J. Genet. 66:317-334(1991).
-!- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR
METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
-:- SIMILARITY: BELONGS TO ADBNIVIL OTCLASE CLASS-3 FAMILY.
-:- SIMILARITY: CONTAINS 23 LEUCINE-RICH REPEATS (LRR).
-:- SIMILARITY: CONTAINS 1 PP2C-LIKE DOMAIN.
                                                                                                                                                                                      Score 34; DB 1; Length 560; Pred. No. 17;
                                                                                                                                                                                                                        15; Indels
                                                                                                                                                     8ECB9F9626FFC40A CRC64;
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                                                                                                                                                                                                                        1; Mismatches
                                 POTENTIAL.
POTENTIAL.
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 POTENTIAL. POTENTIAL.
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InterPro; IPR001614; LRR.
InterPro; IPR001611; LRR.
InterPro; IPR003591; LRR_out.
InterPro; IPR003591; LRR_typ.
InterPro; IPR003591; PP2C-1ike.
InterPro; IPR001932; PP2C-1ike.
InterPro; IPR001932; PP2C-1ike.
InterPro; IPR00193; RA_domain.
Pfam; PF00211; guanylate_cyc; I.
Pfam; PF00560; LRR; 14.
Pfam; PF00788; RA; I.
PRINTS; PR00019; LEURCHRPT.
SMART; SM00044; CYCC; I.
SMART; SM00370; LRR; 4.
SMART; SM00332; PP2CC; I.
                                                                                                                                                                                                                                                       118 LPDXHXXLXXXDXXXYLLXIWXP 140
                                                                                                                                                                                                                                                                             249 LPDITSALVSIVSLALFLKVWRP 271
                                                                                                                                                     58920 MW;
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                                                                                                                                                                        Query Match
Best Local Similarity 30.4%
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 179
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CR-1 OR NAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burton J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE L24P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                  CYCLASES_2; 1.
repeat; cAMP synthesis; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Indels .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52E79B90E6B17A7B CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-Sos ribosomal protein L26.
RPL-26 OR F28G6.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 AA
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PP2C-LIKE.
CATALYTIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%;
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SMART; SM00314; RA; 1.
PROSITE; PS50125; GUANYLATE_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 KXXXXLRTEHXVXXLPDXH 122
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                                 Leucine-rich
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Query Match
Best Local Similarity 31.00,
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335 KGSAKIKTHHNVGGLPE 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- CATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine + H(2)O = AMP + diphosphate + GMP + L-glutamate.
-i- PATHWAY: GMP blooynthesis.
-i- SUBGNIT: HOWODIMER (BY SIMILARITY).
-i- SUBGNIT: HOWODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                               Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
                                                                                                                                                                                                                                                                 Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
6MP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) (Glutamine amidotransferase) (GMP synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF00117; GATASA: 1.
Pfam: PF00117; GATASA: 1.
Pfam: PF00159; AMTSTHRASEII.
PRINTS: PR00099; ANTSTHRASEII.
PRINTS: PR00099; GATASE.
TIGREAMS: TIGRO0884; guaA_Cterm; 1.
PIGREAMS: TIGRO0888; guaA_Nterm; 1.
PROSITE: PS00442; GATASE_TYPE_I; 1.
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GMP-BINDING (BR SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
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InterPro; IPR00991; GATase_I.
InterPro; IPR001674; GMP_synt_C.
InterPro; IPR004739; GMPsynthase_N.
                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98196666; PubMed-9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000679; AAC06558.1; -. HSSP; P04079; 1GPM.
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                                                                                                                 STANDARD;
                      224 TEHSVGFVPD 233
111 TEHXVXXLPD 120
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                                                                                                                                                                                                                                                                                                NCBI_TaxID=63363;
                                                                                                                                                                                                                                                     Aquifex aeolicus
                                                                                                                                                                                                                                   GUAA OR AQ_236.
                                                                                                                                             30-MAY-2000
30-MAY-2000
15-JUN-2002
                                                                                                                GUAA_AQUAE
O66601;
                                                                                                                                                                                                                                                                                                                                                   STRAIN-VF5
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ACT_SITE
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                                                                                                GUAA_AQUAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K12 / MC4100;
MEDLINE-21645912; PubMed=11785976;
MEDLINE-21645912; PubMed=11785976;
MINDEZ M.F., Kwon O., Wilson T.H., Aquilar J., Baldoma L., Lin E.C.C.;
"Transport of L-lactate, D-lactate, and glycolate by the LidP and GlcA membrane carriers of Escherichia coli";
Biochem Biophys. Res. Commun. 290:824-829(2002).
FICHION: Transports glycolate across the membrane. Can also transport L-lactate and D-lactate. Seems to be driven by a proton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF THE STAIN TO STAIN TO STRAIN TO S
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIGHZI Z. MG1655;
STRAIGHZI Z. MG1655;
BATTINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                              Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Inner membrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Probable).
-!- INDUCTION: By glycolate.
-!- SIMILARITY: BELONGS TO THE LACTATE PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             motive force.
                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microbiology 147:1069-1077(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000380; AAC76011.1; -. EcoGene; EG12995; glcA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U28377; AAA69142.1;
   STANDARD;
                                                                                                                                                     Glycolate permease glcA. GLCA OR B2975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION
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                                                                                                                                                                                                                                                                                                       NCBI_TaxID=562;
GLCA_ECOLI
Q46839;
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TRANSMEM
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Gaps

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Length 250;

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                         MURF_TREPA
083401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spirochete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                      MURF_TREPA
                                                Matches
                                                                                                                                                                                                            RESULT 8
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-17. Haino Y., Horikawa H., Yamazaki S., Haikawa Y., Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagal Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
-!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. TDXH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 34; DB 1; Length 249; 50.0%; Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aeropyrum pernix.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antioxidant; Complete proteome.
ACT_SITE 50 50 BY SIMILARITY.
SEQUENCE 250 AA; 28703 MW; 0457F2852D051E7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   03B17D50DBA9EE4B CRC64;
  SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable peroxiredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                     InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf_C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP000064; BAA81290.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000866; AhpC-TSA.
                                                                                                                                                                                                                                                                                                                                                                                                66
28295 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desulfurococcaceae; Aeropyrum NCBI_TaxID=56636;
                                                                                                                                                                                                                                 EMBL; U75930; AAC59088.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00578; AhpC-TSA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 50.0 nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 LRTEHXVXXLPDXH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 LRAERAVKALADAH 206
                                                                                                                                                                                                                                                                                                                                                                                                                   249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                      Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDXH_AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                              ZN_FING
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TDXH_AERPE
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Matches
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15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
UDP-N-acctylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl liqase (EC 6.3.2.15) (UDP-MurNAc-pentapeptide synthetase)
(D-alanyl-D-alanine-adding enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glutamyl-meso-2.6-diaminoheptanediodte + D-alanyl-D-alanine = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-6-carboxy-L-lysyl-D-alanyl-D-alanine.
-!- PATHWAY: Peptidoglycan blosynthesis.
-!- PATHWAY: Peptidoglycan blosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- FUNCTION: INVOLVED IN CELL WALL FORMATION. CATALYSES THE FINAL STEP IN THE SYNTHESIS OF UDP-N-ACETYLMURAMOYL-PENTAPEPTIDE, THE PRECURSOR OF MUREIN (BY SIMILARITY).

-1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOY1-L-ALANY1-D-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01225; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase_C; 1.
TIGRPAMs; TIGR01143; murF; 1.
Peptidoglycan synthesis; Cell division; Cell wall; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 459;
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).
23EA5571ED95F332 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spirochaetales; Spirochaetaceae; Treponema.
Score 34; DB 1;
Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8%; Score 34; DB 1;
60.0%; Pred. No. 14;
Live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             459 AA
                                                                     Mismatches
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Interpro; IPR004101; Mur_ligase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
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NP_BIND 121 127
SEQUENCE 459 AA; 50234 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
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5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 281:375-388(1998).
                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                       111 TEHXVXXLPDXH 122
                                                                                                                                                                                                      19 TDHGVIKLPDHY 30
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TIGR; TP0386; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treponema pallidum.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=160;
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VCG3_NPVOP
010339;
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                                                                                                                                                                                genes.
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         SOUR PRESENTATION OF THE PRESENT OF 
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JR EMBL, AL627276; C.L.

JR EMBL; AL8668.

DR PIR; A28668.

DR Stydene; SG10237; muts.

DR Stydene; SG10237; muts.

DR InterPro; IPR000432; Muts_C.

DR InterPro; IPR002863; Muts_C.

DR InterPro; IPR002863; Muts_C.

DR TGRPAMS; TGR01070; muts]; 1.

DR TGR01070; 1.

DR TGR0107
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"PIKI, an essential phosphatidylinositol 4-kinase associated with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Planagan C.A., Schnieders E.A., Emerick A.W., Kunisawa R., Admon A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thorner J.; "Phosphatidylinositol 4-kinase: gene structure and requirement for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
   step. This protein has a weak ATPase activity.
SIMILARIT: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
SAUTION: Ref.1 sequence differs from that shown due to frameshifts in positions 353, 379, 394, 422 and 425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
Phosphatidylinositol 4-kinase PIK1 (EC 2.7.1.67) (PI4-kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1066 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                   EMBL, U16303; AAA80578.1; ALT_FRAME.
EMBL, M18965; AAA27167.1; ALT_FRAME.
EMBL, AE008832; AAL21789.1; --
EMBL, AL627276; CAD06015.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=94069320; Pubmed-8248783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94252322; Pubmed-8194527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 КМКНАРООГРЕГНАОГЕТУВ 388
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Science 262:1444-1448(1993).
[3]
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EMBO J. 13:2352-2361(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Ptdīns-4-kinase).
PIK1 OR YNL267W OR N0795.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIK1_YEAST
P39104;
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PIK1_YEAST
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SEQUENCE FROM N.A. STAALN-STAALN-STABC / FY1679; MEDLINE-96310631; PubMed-8740425; MEDLINE-96310631; PubMed-8740425; Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.; "The sequence of a 24,152 bp segment from the left arm of chromosome XIV from Saccharomyces cerevisiae between the BNI1 and the POL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                          FUNCTION: ACTS ON PHOSPHATIDYLINOSITOL (PI) IN THE FIRST COMMITTED STEP IN THE PRODUCTION OF THE SECOND MESSENGER INOSITOL-1, 4,5,-TRISPHOSPHATE. PIX1 IS PART OF A NUCLEAR PHOSPHOINOSITIDE CYCLE AND COULD CONTROL CYTOKINESIS THROUGH THE ACTIN CYTOSKELETON.

CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol = ADP
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Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R EMBL, 271543; CAA96174.1; -.

R PIR; A44335; A49335.

R PIR; A4456.5 s44456.

R InterPro; IPR000403; PI3_PI4_kinase.

R InterPro; IPR00046; PI3_PI4_kinase.

R PROSITE; PS00916; PI3_4 KINASE.1; 1.

R PROSITE; PS00916; PI3_4 KINASE.2; 1.

R PROSITE; PS029016; PI3_4 KINASE.2; 1.

R PROSITE; PS029016; PI3_4 KINASE.2; 1.

R PROSITE; PS029016; PI3_4 KINASE.3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 1; Length 1066; Pred. No. 12;
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-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X76058; CAA53658.1; -. EMBL; L20220; AAA34873.1; -. EMBL; X92494; CAA63231.1; -. EMBL; Z71543; CAA96174.1; -.
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nes 5; Conservative
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                                                                                                                                                                                                                                                                                    Yeast 12:505-514(1996).
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110 RTEHXVXXLPDXH 122
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                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
THE C-TERMINAL FRAGMENT CONTAINING THE SPACER 2 AND THE FOUR TS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R InterPro; IPR001762; Disintegrin.
R InterPro; IPR001801762; Disintegrin.
R InterPro; IPR001801762; Reprolysin.
R InterPro; IPR001804; TSP1.
R InterPro; IPR001804; TSP1.
R InterPro; IPR001804; TSP1.
R InterPro; IPR001804; TSP1.
R Pfam; PF001802; PSP1; 6
R Pfam; PF001802; PSP1; 8.
R PR01187; SM00209; TSP1; 8.
R PR051TE; PS00025; TSP1; 8.
R PR051TE; PS000427; DISINTEGRIN_1; FALSE_NEG.
R PR051TE; PS000427; DISINTEGRIN_1; FALSE_NEG.
R PR051TE; PS00142; TSP1; 2.
R PR051TE; PS00142; ZINC_PR0TEASE; 1.
R PR051TE; PS00142; ZINC_PR0TEASE; 1.
R PR051TE; PS00142; ZINC_PR051EASE; 2.
R P001425 ZINC_PR051EASE; 2.
R P001425 ZINC_PR051EASE; 2.
R P001
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BY SIMILARITY.
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                                                  SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B. SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN. SIMILARITY: CONTAINS 8 TSP TYPE-1 DOMAINS.
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TSP TYPE 1 3.
TSP TYPE 1 4.
SPACER 2.
TSP TYPE 1 5.
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TSP TYPE 1 7.
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N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPACER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ250725; CAC20419.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                         HGNC:14605; ADAMTS12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.3%;
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1104
1275
1320
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392
393
396
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105
125
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                                                                                                                                                                                                                                                                                                                                                                                                                                   606184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
METAL
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
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SEQUENCE
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CHAIN
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DOMAIN
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Gaps

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Indels

Pred. No. 11;

46.28;

Best Local Similarity

Conservative

9

Matches

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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                              SPECIES-S.typhimurium;
MEDLINE-88086868; PubMed=3275609;
Haber L.T., Pang P.P., Sobell D.I., Mankovich J.A., Walker G.C.;
"Nucleotide sequence of the Salmonella typhimurium muts gene required for mismatch repair: homology of Muts and HexA of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Materston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Detecting frame shifts by amino acid sequence comparison.";
J. Mol. Biol. 234:1140-1157(1993).
-!- FUNCTION: This protein is involved in the repair of mismatches in DNA. It is possible that it carries out the mismatch recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haber L.T., Walker G.C.;
"Altering the conserved nucleotide binding motif in the Salmonella typhimurium MutS mismatch repair protein affects both its ATPase and mismatch binding activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."; Nature 413:848-852(2001).
                                                                                                                                                                                                                                            Salmonella typhimurium, and
Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION OF PROBABLE FRAMESHIFT IN 394-425
                                                                                                                                                                     (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                             855 AA
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 1-5
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-S.typhi; STRAIN-CT18;
MEDLINE-21534947; Pubmed-11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=S.typhimurium;
MEDLINE=91330898; PubMed=1651234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=S.typhimurium;
MEDLINE=94087727; PubMed=7903399;
                                                                                                                                                                                                     DNA mismatch repair protein muts MUTS OR STM2909 OR STY3033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eumoniae.";
Bacteriol. 170:197-202(1988)
                                                                                                                                                 01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTAGENESIS, AND ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 10:2707-2715(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:852-856(2001).
                                                                                                             STANDARD;
| || : ||: |
RQEHFIKGLPEYH 53
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=602, 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                     15-JUN-2002
                                                                                                                                                                                       15-JUN-2002
                                                                                                                                                                                                                                                                                                        Salmonella.
                                                                                                           MUTS_SALTY
P10339;
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us-09-840-743-73.rsp

SUBCELLULAR LOCATION: CYTOPLASMIC. PROBABLY BINDS INDIRECTLY TO THE INNER PLASMA MEMBRANE.

INTERMEDIATE AND LIGHT CHAINS

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δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
 A Squros J. Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Radooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Rad Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA James K., Jones L., Sunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Ratherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Radolfens I., Vanstreels E., Reger M., Malsh S.V., Warren T., Whitehead S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
Radolfens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
R. Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
R. Beer P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
R. Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
R. Langer R., Strobert M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
R. Dominguez A., Revuelta J.L., Jimene J., Sanchez M., Galzon R.,
R. Boaga R.R., Cruzado L., Jimene J., Sanchez M., Galzon R.,
R. Boninguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.,
R. The genome sequence of Schizosaccharomyces pombe.";
R. Patter 41581-880(2002)
                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS A MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND
                                                                                                                                                                         Gaps
                                                                    D (GLCNAC. .) (POTENTIAL).
D (GLCNAC. .) (POTENTIAL).
SECRETION FROM ER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES ARGUMENTELES ALONG MICROTUBULES. REQUIRED FOR NUCLEAR MOVEMENT
                                                     N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                         ;
                                                                                                                                            Score 41; DB 1; Length 1548;
                                                                                                               95D6849961622DB6 CRC64;
                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto A., West R.R., McIntosh J.R., Hiraoka Y.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                           UDP-GLUCOSE: GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                           Dynein heavy chain, cytosolic (DYHC).
DHC1 OR SPAC30C2.01C OR SPAC1093.06C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungl; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetae;
                                         GLUCOSYLTRANSFERASE.
                                                                                                                                                                                                                     96 PXXXXXXXXXXXXLRTEHXVXXLPDXHXXLXXXXXXXXI 134
                                                                                                                                                                                                                                                                                                     DYHC_SCHPO STANDARD; PRT; 4196 AA. 013290; Q996L0; Q9UTPB; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                        2; Mismatches
                                                                                                                                                           Pred. No. 1
                                                                                                 PREVENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21848401; PubMed-11859360;
                                                                                                                                            6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DURING MEIOTIC PROPHASE.
                                                                                                               1548 AA; 174465
                                                                                                                                                                         11; Conservative
                                                     181
266
864
1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                     181
266
864
                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CRL152;
Glycoprotein.
                                                                    CARBOHYD
                                                       CARBOHYD
                                                                                                               SEQUENCE
                                                                                                                                            Query Match
             SIGNAL
                           CHAIN
                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                         DYHC_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>;</u>
                                                                                                                                                                                                                                                                           RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUT THE THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.
PTM: IS SUBJECTED TO AN INTRACELLULAR MATURATION PROCESS LEADIND
TO A FRAGMENT CONTAINING THE N-TERMINAL REGION INCLUDING THE
METALLOPROTEINASE, DISINTEGRIN-LIKE, CYS-RICH AND TS-1 DOMAINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matrix (By similarity).
-!- TISSUE SPECIFICITY: Expressed exclusively in fetal lung. Is widely
expressed in gastric carcinomas and in cancer cells of diverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                origin.

DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
45-JUN-2002 (Rel. 41, Last annotation update)
metalloprocteinase with thrombospondin motifs 12) (ADAM-TS 12) (ADAM-
                                                                                                                                                                           EMBL; AB005784; BAA22056.1; -..

R EMBL; AB35852; CAB90788.1; -..

AR EMBL; AL132839; CAB60551.1; -..

AR Motor protein; Microtubules; Dynein; ATP-binding; Coiled Coil.

FT DOMAIN 1217 1252 COILED COIL (POTENTIAL).

FT DOMAIN 1984 2012 MICROTUBULE-BINDING (POTENTIAL).

S315 3403 COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 1; Length 4196;
SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8F10AE370184FC0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484308 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1140 SEHLENBEDDTHSSLSTVD 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 TEHXVXXLPDXHXXLXXXD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 36.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2176
2181
2527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2169
2174
2520
4196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AT12_HUMAN
P58397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Sat Noy

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

protein - protein search, using sw model ŏ

2002, 19:24:14 8 November Run on:

; Search time 10.4967 Seconds (without alignments) 1153.796 Million cell updates/sec

US-09-840-743-73

Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 segs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed DB Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	32 d		P58397 homo sapien	P10339 salmonella	P39104 saccharomyc	Ol0339 orgyia pseu	Q9y910 aeropyrum p	treponema	)l aquifex ae	Q46839 escherichia	Q01631 neurospora	Q19869 caenorhabdi	_		Q9pe52 xylella fas		Q00461 fremyella d	~			myxoc	Q01484 homo sapien	3 zymom	Q9n4d6 caenorhabdi	Q24192 drosophila	~	P44689 haemophilus	Q10990 schizosacch	P77377 escherichia	Q99829 homo sapien	_	Q13651 homo sapien	Q59934 streptococc
SUMMARIES		ID	UGGG_DROME	DYHC_SCHPO	AT12_HUMAN	MUTS_SALTY	PIK1_YEAST	VCG3_NPVOP	TDXH_AERPE	MURF_TREPA	GUAA_AQUAE	GLCA_ECOL1	CYAA_NEUCR	RL26_CAEEL	TDXH_PYRAB	- 1	RPOA_XYLFA	DVR1_BRARE	T701_FREDI	DRTS_TRYCR	TSCC_PSEAM	RP16_DROME	RFBC_MYXXA	ANK2_HUMAN	TYRC_ZYMMO	SEST_CAEEL	RHOL_DROME	RFAY_SALTY	MESJ_HAEIN	YE0J_SCHPO	WZXC_ECOLI	CNE1_HUMAN	HEXA_CAEEL	I10R_HUMAN	PFL_STRMU
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di	Query	Match		٠.	6.3	6.1	6.1		٠											٠.			5.6				5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4
		Score	41	38	37	36	36	34	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33	c	32.5	'n	32	32	32	32	32	32	32	32	32
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or send an email to license@isb-sib.ch).

EMBL; U20554; AAA85850.1;

Flyase; FBgn0014075; Ugt. Interpro; IPR002495; GT\_8. Pfam; PF01501; Glyco\_transf\_8; 1. Signal; Transferase; Glycosyltransferase; Endoplasmic reticulum;

032797 lactococcus	032799 lactococcus	P41511 ustilago ma	Q61789 mus musculu	O30409 b tyrocidin	P42672 avian adeno	Q45557 bacillus sp	P55618 rhizobium s	026518 methanobact	Q44470 agrobacteri	P70786 agrobacteri	Q01767 streptomyce	
PFL_LACLA	PFL_LACLC	TOP1_USTMA	LMA3_MOUSE	TYCC_BACBR	ADEN_ADEG1	TRUA_BACSP	Y4PM_RHISN	APG2_METTH	TUB4_AGRVI	TUB3_AGRVI	LAT_STRCL	
Η,	<b>-</b>	~	٦	П	П	Н	Н	Н	Н	Н	П	
787	/8/	1019	2569	6486	206	244	272	402	433	449	457	
4.	5.4	5.4	5.4	5.4	5.3	5.3	5.3	5.3	5.3	5.3	5.3	
32	3.5	32	32	32	31	31	31	31	31	31	31	
34	35	36	3.7	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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THE EARLIEST EMBRYOS, INCLEASING AT 6-8 HRS WITH A MAXIMUM AT 10-12 HRS. LEVELS DECREASING AT 6-8 HRS WITH A MAXIMUM AT 10-12 HRS. LEVELS DECREASE THERRAFTER AND ARE NOT DETECTED IN 18-20 SECOND INSTAR TO PUPATION.

SIMILARIY: SOME, TO YEAST KRES, S.TYPHIMURIUM RFAJ AND E.COLI RFAI PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: UNFOLDED, DENATURED GLYCOPROTEINS ARE SUBSTANTIALLY BETTER SUBSTRATES FOR GLUCOSYLATION BY THIS ENZYME THAN ARE THE CORRESPONDING NATIVE PROTEINS. THIS PROTEIN AND TRANSIENT GLUCOSYLATION MAY BE INVOLVED IN MONITORING AND/OR ASSISTING THE FOLDING AND ASSEMBLY OF NEWLY MADE GLYCOPROTEINS, IN ORDER TO IDENTIFY GLYCOPROTEINS THAT NEED ASSISTANCE IN FOLDING FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- COFACTOR: REQUIRES CALCIUM AND MANGANESE IONS FOR ACTIVITY.
-i- PATHAAY: Glycosylation.
-i- SUBUNIT: MONOMER.
-i- SUBCELLULAR LOCATION: Endoplasmic reticulum.
-i- DEVELOPMENTAL STAGE: IS PRESENT AT LOW BUT DETECTABLE LEVELS IN
                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
10P-91ucose:91ycoprotein glucosyltransferase precursor (EC 2.4.1.-)
(UDP-Glc:91ycoprotein glucosyltransferase) (dUGT).
                                                                                                                                                                                                                                                                               TISSUE=Embryo;
MEDLINE=95246722; PubMed=7729408;
MEDLINE=95246722; PubMed=7729408;
Parker C.G. Fessler L.I., Nelson R.E., Fessler J.H.;
"Drosophila UDP-glucose:glycoprotein glucosyltransferase: sequence and characterization of an erzyme that distinguishes between
                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoc
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 PRT; 1548 AA
                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 23-37.
                                                                                                                                                                                                                                                                                                                                                                            denatured and native proteins.";
EMBO J. 14:1294-1303(1995).
 STANDARD;
                                                                                                                                                                                                                               NCBI_TaxID=7227;
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                                    01-NOV-1997
01-NOV-1997
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UGGG_DROME
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7. 6

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395 ACAGTICIGCITITGGAAAGGATTCGTATGTGTCCGTGGATTCGAACAGAAGACAAAGAGC 336
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Alarge scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                      EST 06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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6365 gagaggaagttttccgctcaacgggacatatttccaagtcaacgagttatttgcagacca
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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/organism="Arabidopsis thallana"
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Pred. No. 4.7e-68;
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759 bp mRNA linear EST 31-JAN-2001
EST469495 tomato shoot/meristem Lycopersicon esculentum cDNA clone
CTOF3624 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon esculentum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                     6724
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van der Hoeven, R. Bezzerides, J., Sun, H., Cho, J., Utterback, T.,
Hansen, C., Ronning, C. and Tanksley, S.
Generation of ESTs from tomato shoot/meristem tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="crop3624"
/clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
1.0ation/Qualifiers
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/cultivar="TA496"
/db_xref="taxon:4081"
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Pred. No. 3.5e-57;
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Best Local Similarity 73.4
Matches 524; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
                                          1 (bases 1 to 500)
Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K., Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and
             tttgatcatggtgctcatcagggcgttaccaacttaagtatgatgatcaatagcttagcg 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis Genomic Sequencing. Update Unpublished (1997)
Contact: Steve Rounsley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A BAC End Sequence Database for Identifying Minimal Overlaps in
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rounsley@tigr.org
Seq primer: M13-21
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Medical Center Dr., Rockville,
301 838 0200
301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 500.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="T1907"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="hermaphrodite"
/sex="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII
/note="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII
; Produced by Rod Wing"
; Produced by Rod Wing"
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99.2%;
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Pred. No. 9.6e-71;
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1 (bases 1 to 486)
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Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Eukaryotic Genomics
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of 12,028 non-redundant expressed sequence tags from normalized and DNA Res. 7, 175-180 (2000)

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers

/organism="Arabidopsis thaliana"

/db\_xref-"taxon:3702"

/clone-"SQ049d09F" /strain="Columbia

The First Laboratory for Plant Gene Research Kazusa DNA Research Institute

20363093 Contact: Erika Asamizu

/clone\_lib="Arabidopsis thaliana green siliques Columbia'

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0; Mismatches 1;

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    /organism="Arabidopsis thallana"

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ORGANISM

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SOURCE

REFERENCE AUTHORS

Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 527)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.

v 0 v 0 0 v 0 0 v

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences Release 5.4

Results file seq72-t48453.res made

by bobryen on Tue 17 Dec 102 12:58:03-PST

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Similarity matrix PA
Threshold level of sim.
Mismatch penalty
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The list of best scores is:

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61
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283224

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_73:\*

Database

283224 seqs, 96134422 residues

Searched:

Scoring table:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 2
106430

Hypothetical protein F28A23.180 - Arabidopsis thaliana
C;Species: Arabidogsis thaliana (mouse-ear cress)
C;Species: Arabidogsis thaliana (mouse-ear cress)
C;Accession: 105430
R;Bevan, M; Weichselgarther, M; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A. submitted to the Protein Sequence Database, October 1998
A;Reference number: Z15415
A;Rocession: T05430
A;Molecule type: DNA
A;References: EMBL:AL021961
A;Experimental source: cultivar Columbia; BAC clone F28A23

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RESULT 3
T48452
hypothetical protein T32M21.160 - Arabidopsis thaliana
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C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T48452
N : Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Cl
                                                                                                                                                                   R:KUNST, F: Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cha A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler Lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueely, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot A.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, R.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Ritle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A.; Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C;Accession: E69958
                                                            A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-442 <KUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, March 2000 A;Reference number: Z24487 A;Accession: T48452
                                                                                                                                                  A; Accession: E69958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein yahB - Bacillus subtilis
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A; Introns: 167/1; A; Note: T32M21.160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; McJecule type: DNA
A; Residues: 1-1017 <BEV>
A; Cross references: EMBL: AL162875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
           Cross-references: GB:Z99116; GB:AL009126; NID:g2634723; Qerimental source: strain 168
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17; Conservative
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28.8%;
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Pred. No. 5;
0; Mismatches
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Pred. No. 3.3e-19;
0; Mismatches 47
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                         PIDN:CAB14406.1; PID:g2634909
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RESULT
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Query Match
Best Local Similarity
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                                                                                                                                          A;Gene: UU557
A;Genetic code:
                                                                                                                                                                                           A;Cross-references: GB:AE002154; GB:AF222894; NID:g6899557; A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-1131 <GLA>
                                                                                                                                                                                                                                                                              A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views A;Reference number: A82870
A;Accession: F82875
                                                                                                                                                                                                                                                                                                                                 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, submitted to GenBank, February 2000
                                                                                                                                                                                                                                                                                                                                                                                 C; Date: 18-Aug-2000 #sequence_revision
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C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
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A;Gene: yghB
C;Superfamily: hypothetical protein HI0107
                                                                                                                                                                                                                                                            A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein UU557 [imported] - Ureaplasma urealyticum
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A;Introns: 45/1; 105/2; 199/3; 303/2; 382/3; 503/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-541 <WIL>
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Best Local Similarity
   744
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                                  54 FXXWKGSVVDSVXGVFLT 71
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FDKYAGSTYDSALGLFLT 761
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11; Conserv
                                                                      Conservative
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50.0%;
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28.2%;
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ZK892
                                                                                   Score 45;
Pred. No.
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Pred. No. 5.
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                                                                      Mismatches
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                                                                                                    Length 1131;
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Page

71

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

- protein search, using sw model OM protein

Run on:

2002, 19:24:14 ; Search time 5.88235 Seconds æ November

(without alignments)
1470.857 Million cell updates/sec

US-09-840-743-71 Perfect score:

1 KVXXDXXTXXXWXXLXXXXD.........TQNXDXXSSXAXMXXAXXFP 90 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters: seq length: 0 : seq length: 200000000 Minimum DB Maximum DB

283224

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
1: pir3:\*
: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote hypothetical prote hypothetical prote hypothetical prote unknown protein T1 hypothetical prote hypothetical prote hypothetical prote alpha-mannosidase-HIVD family secret probable periplasm aminopeptidase N V probable phosphopr hypothetical prote early protein gp13 early protein gp13 early protein gp13 hypothetical prote hypothetical prote conserved hypothet hypothetical prote acyltransferase, p endonuclease III-r hypothetical prote hypothetical prote hemolysin homolog conserved hypothet Description SUMMARIES C96748 G83962 T29718 H72278 AE2799 G97578 G82193 T01385 T30094 WRBP13 JN0031 D81052 G69199 T48452 E69958 T28069 F82875 T06602 AH1353 AI1723 F69826 F24676 H69874 Length DB 4444 638 638 637 637 638 638 638 638 638 638 Query Match 163.5 162 49.5 Score 43.5 43.5 Result No. 

Cydrocasion: T05430
R;Bevan, M.; Weichselgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A. submitted to the Protein Sequence Database, October 1998
A;Reference number: Z15415
A;Reference number: Z15415
A;Reference number: Z15410
A;Molecule type: DNA
A;Reference number: DNA
A;Reference number: Z15410
A;

hypothetical prote

hypothetical protein F28A23.180 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr\_1999 #sequence\_revision 23-Apr-1999 #text\_change 24-Nov-1999

myosin IC - slime	RNA polymerase bet	probable lectin pr	gellan lyase (EC 4	preprotein translo	conserved hypothet	hypothetical prote	spou rRNA methylas	probable sugar ABC	citrate (si)-synth	citrate synthase,	glucan 1,4-alpha-g	hypothetical prote	probable heterochr	WD-40 repeat prote	hypothetical prote
T30578	S73652	T40912	T00047	E95237	F98101	B72776	687396	AG0404	S41563	T49379	T49633	T23238	T37916	AC2239	T00637
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1181	1391	312	2475	66	66	128	263	329	469	469	748	196	960	1526	1922
14.9	14.9	14.7	14.7	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5
41	41	40.5	40.5	40	40	40	40	40	40	40	40	40	40	40	40
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

hypoth C;Spec C;Date	hypothetical protein At2g36490 [imported] - Arabidopsis thallana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: D84781
R; Lir M.; F	R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallo
euss, Natuı	D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vere 402, 761-768, 1999
A;Tit A;Ref	A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487; PMID:10617197
A; AC( A; Sta A; Mo]	A;Accession: D84781 A;Status: preliminary A;Molecule type: DNA
A; Res A; Crc C; Ger	A.Residues: 1-1207 <sto> X.ross-references: GB:AE002093; NID:g4581149; PIDN:AAD24633.1; GSPDB:GN00139 C:Genetics:</sto>
A;Ger A;Mar	A;Gene: At2g36490 A;Map position: 2
Que	Query Match 59.5%; Score 163.5; DB 2; Length 1207; Best Local Similarity 43.4%; Pred. No. 2.5e-19; Matches 43: Conservative 0: Mismatches 47: Indels 9: Gans 2:
δý	XXXXDXXXXXXXXXERXXFXXRXXXFIXRMXXXQGXR 52
QQ	500 KVDLDDETDRVWKLLLENINSEGVDGSDEQKAKWWEEERNVFRGRADSFIARMHLVQGDR 559
Οy	53 XFXXWKGSVVDSVXGVPLTQN-XDXXSSXAXMXXAXXFP 90
QQ	560 RFTPWKGSVVDSVVGVFLTQNVSDHLSSSAFMSLASQFP 598

on, cer

IntelliGenetics

Results file seq72-q941x6.res made by bobryen on Tue 17 Dec 102 12:58:40-PST.

FastDB - Fast Pairwise Comparison of Sequences Release 5.4

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Similarity matrix py
Threshold level of sim.
Mismatch penalty
Gap penalty
Gap size penalty
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Number of sequences searched:
5
Number of scores above cutoff:
5
Number of residues:
Number of sequences searched:
Number of scores above cutoff:
                                               Times:
                                                                                                          Cutoff score
Randomization group
                                                                         Scores:
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132
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The scores below are sorted by initial score. Significance is calculated based on initial score.

Initial Score Residue Identity - Gaps

93 60% 1

Optimized Score = 115
Matches = 72
Conservative Substitutions

115 Significance - 72 Mismatches - 110ns

0.65 46

70

3. に知る方式で Q941x6 (1-132) Putative FPPsynthasel (Fragment).

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

130 X LPXXQXHX           LPESIQLHLLEL 550 X	60 70 90 100 120 LXXXVXXHGXIDLEWLRXXPPDXAKXILLSIXXLGLKSVECVRLLXLHXXAFPVDIN-GRIAVRLGWVPLQP	X 10 20 30 40 50 WXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	Initial Score 9 Optimized Score 119 Significance 0.73 Residue Identity 54 Matches 73 Mismatches 58 Gaps 1 Conservative Substitutions 1	2. SEQ72-Q941X6 (1-132) t48453 TQIG_Gf:_t48453 check: 2431 from: 1 to: 555	130 X LPXXXQXHX	60 70 80 90 100 110  LXXXVXXHGXIDLEWLRXXPPDXAKXYLLSIXGLGLKSVECVRLLXLHXX3EPVDIN-GRIAVRLGWVPLQP	X 10 30 40 AV 10 30 AV 10 AV 1	Initial Score = 100 Optimized Score = 121 Significance = 0.84 Residue Identity = 56% Matches = 75 Mismatches = 57 Gaps = 1 Conservative Substitutions = 0	1. SEQ72-Q941X6 (1-132) q9sr66 T22K18.18 protein.	1. q9sr66 T22Kl8.18 protein. 1309 100 121 0.84 2. t48453 TOTG of: t48453 check: 2431 555 96 119 0.73 2. t48453 Putative FPPsynthasel (Fragme 119 93 115 0.65	Init. Opt. Score Score Sig.
	<b>v — v</b>	aj — aj				<b>v−v</b>	<b>4)</b> — 4)			000	ı Di

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119 AA; 13771 MW; FBDBCE4CD0CC5B81 CRC64;

119

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Asada T., Fukusaki E., Kobayashi A., Sando T.;
"Prenyltransferase of Euphorbia tirucalli.";
Submitted (NOV-2000) to the EmBL/GenBank/DDBJ databases.
InterPro; IPR002265; Endo_3c.
InterPro; IPR003265; Endo_3c.
Pfam; PF00730; HHH-GPD; 1.
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SEQUENCE
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                                 930
                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudigotyledons; Core eudicots; Rosidae;
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 DSIDYEAIRRASISEISEAIKERGMNNMLAVRI------KDFLERIVKDHGGIDLE 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 WLRXXXXXX¥KXXLLXXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXPLP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||
| 486 WLRESPPDKAKDYLLSIRGLGIKSVECVRLLTLHNLAFPVDTNVGRIAVRMGWVPLQPLP 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bevan M., Terryn N., Ardiles W./, Buysshaert C., Dasseville R.,
De Clerck R., De Keyser A., Next P., Rouze P., Van Den Daele H.,
Villaroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.,
Submitted (MAR-2000) to the FEMBL/GenBank/DDBJ databases.
                                     157 XLWPRICKLXQXTLYELHYXXIIFGKXXFCTKXXPNCNACPMXXXCXXXXSA 209
                                                       32.9%; Score 228; DB 10; Length 555; 44.5%; Pred. No. 1.6e-29;
EU Arabidopsis sequencing/project,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL162875; CAB85563/1;
Interpro; IPR003265; Endo_3c.
Pfam; PF00730; HhH-GPD/1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $2088 MW; A1B44BDDE17FDC1E CRC64;
                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UJNV-2002 (TrEMBLrel. 21, Last sequence update)
Hypothetical 62.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
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0; Mismatches
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Matches 57; Conset/ative
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Hypothetical protein,
SEQUENCE 555 AA; #20
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 17, Last annotation update)
Hypothetical 106.3 Map protein.
F28A23.180 OR AT4G34060.
Arabldopsis thaliana (Mouse-ear cress).
Eukaryota, Virid plantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Maplantae; Streptophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Erasaicales; Brassicaceae; Arabidopsis. 37 IXXRGXXXXLXXRIXXXXXXXXXXXXFLXXXVXXXGXIDLEWLRXXXXXXXXXXXLXXXG 96 31 IKBRGMNNVLAKRI------KDFLNRLVREHGNIDLEWLRDVPPDKAKEYLLSIRG 80 (PXXXXXQKXLWPRLCKLXQXTLYELHYX 1.76 Ġ. -----YELHYQ 661 Herzl A. Gaps Bevan M., Weichselgartner M., Fartmann B., Granderath K., Dauner Herzl A., Neumann S., Hoheisel J., Jesse T., Heijnen L., Vos P., Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. 10; DB 10; Length 917; SEQUENCE FROM N.A.
Weichselgartner M., Fartmann B., Granderath K., Dauner D.,
Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AL021961; CAA17566.1; EMBL; AL161584; CAB80123.1; InterPro; IPR003265; Endo\_3c. InterPro; IPR003565; FeS\_bind Indels 02B3770ACE1A454 CRC64; Score 202; DB 10; Pred. No. 8.1e-26; 0; Mismatches 39; 97 XGLKSXECVRLLXLXXXAFPVDTNVGRIXVRXGXVPLXP 135 29.1%; Scord 201.5; DB 10; 49.5%; Pred No. 7.8e-25; tive 0; Mismatches 22; 662 MITFGK-VFCTKTIPNCNACPM-KSECKYFASA 692 177 XITFGKXXFCTKXXPNCNACPMXXXECXXXXSA 625 VDTNVGRIAVRLGLVPLEPLPNGVQMHQLFE-117 VDTNVGRIXVRXGXVPLXPLPXXXQXHXLXX 29.1%; 50.5%; Hypothetical protein. SEQUENCE 917 AA; 106310 MW; Conservative PRELIMINARY; SMART; SM00478; ENDO3c; 1. SMART; SM00525; FES; 1. Conservative Similarity SEQUENCE FROM N.A. SEQUENCE FROM N.A. Local Similarity ses 46; Conserv Local St. 50; 049498 Query Match Matches ò g δ

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
WOB TaxID-142860;

01-DEC-2001 (TrEWBLrel. 19, Created) 01-DEC-2001 (TrEWBLrel. 19, Last sequence update) 01-JUN-2002 (TrEWBLrel. 21, Last annotation update) Putative FPPSynthasel (Fragment).

Euphorbia tirucalli.

NEENCE FROM N.A.

119 AA.

PRELIMINARY;

094LX6 Q94LX6

IntelliGenetics

Query sequence being compared: SEQ71-O49498 (1-90)
Number of sequences searched:
4
Number of scores above cutoff:

Results file seq71-o49498.res made by bobryen on Tue 17 Dec 102 12:55:59-PST.

FastDB - Fast Pairwise Comparison of Sequences Release 5.4

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Similarity matrix PAThreshold level of sim. Mismatch penalty Gap penalty Gap size penalty Cutoff score Randomization group
                                                                                                                                                                                          SCORE
STDEV
Number of residues:
Number of sequences searched:
Number of scores above cutoff:
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The list of best scores is:

A 100% identical sequence to the query sequence was not found.

The scores below are sorted by initial score. Significance is calculated based on initial score.

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Herzl

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995360

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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Vintdiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418 KVNLDPETIKEWDVLMVNDSPSRSYDDKETEAKWKKEREIFQTRIDLFINRMHRLOGNRK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KVXXDXXTXXXWXXL-----XXXXDXXXXXXXXXXXERXXFXXRXXXFIXRMXXXQGXRX 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R., Glelen J., Van Montagu M., Bancroft I., Mewes H.W. Rudd S., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112139 MW; 4F7C313A891EC83F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL162875; CAR85562.1;
                                                                                                                                                                                                                         EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO19161; CAA17566.1; -..
EMBL; ALI61584; CAB80123.1; -.
InterPro; IPR003545; Endo_3c.
InterPro; IPR003545; Eos. bind.
PF00730; HhH-GPD; 1.
Mowes H.W., Mayer K., Schueller C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                             SEQUENCE FROM N.A.
Welchselgartner M., Fartmann B., Granderath K., Dauner I
Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                11 protein.
917 AA; 106310 MW; 302B3770ACE1A454 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (PrEMBLrel. 15, Created)
01-0CT-2000 (PrEMBLrel. 15, Last sequence update)
01-0CT-2000 (FrEMBLrel. 15, Last annotation update)
Hypothetical 12.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 162; DB 10;
Pred. No. 1.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FKQWKGSVVDSVVGVFLTQNTTDYLSSNAFMSVAAKFP 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 FXXWKGSVVDSVXGVFLTQN-XDXXSSXAXMXXAXXFP 90
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SMART; SM00525; FES; 1.
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Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
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MEDLINE=20083487; Pubmed=10617197;

MEDLINE=20083487; Pubmed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowmhn C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carreara A.J., Careasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.; the plant Arabidopsis

thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 106.3 kDa protein.
F28A23.180 OR AT4634060.
Arabidopsis thaliana (Mouse-aar cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                         Eukaryophyta; Tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Usidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Bevan M., Weichselgartner M., Fartmann B., Granderath K., Dauner D.,
Erzl A., Neumann S., Hoheisel J., Jesse T., Heijnen L., Vos P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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135$16 MW; ADDB6C9EE94DDF67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006919; AAD24633.1; -. InterPro: JRR003651; Fes. Blind.
SMART; SM00525; Fes. 1.
SQUENCE 1207 AA; 135916 MW; ADDB6C9EE94DDF67 CRC64;
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Last sequence update)
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Pred. No. 9.7e-20;
0; Mismatches 47;
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                    917 AA.
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1 Similarity 43.4%;
43; Conservative (
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Best Local Similarity
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